

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:07:21 ; Search time 179 Seconds
(without alignments)
1407,503 Million cell updates/sec

Title: US-10-756-778-8

Perfect score: 2560
Sequence: 1 IAEPPSTGVITOPRIINDNF.....KLGSQKGEPAIDSIIFSPV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2560	100.0	742	2	068U02
2	2473	96.6	723	2	09EV02
3	244	9.5	829	2	06BE06
4	230	9.0	825	2	06BE09
5	228.5	8.9	1138	1	003749 bacillus th
6	225.5	8.8	1138	1	045707 bacillus th
7	223.5	8.7	1169	1	006014 bacillus th
8	219.5	8.6	1138	1	045708 bacillus th
9	214.5	8.4	645	2	06BE03
10	211.5	8.3	810	2	06BE03
11	210.5	8.2	1167	1	045738 bacillus th
12	207.5	8.1	1169	1	045377 bacillus th
13	207.5	8.1	1174	2	045749 bacillus th
14	207	8.1	660	2	06R006
15	200	7.8	1174	2	06R006
16	198	7.7	1154	2	06QAN9
17	197	7.7	1157	1	06QAN9
18	196	7.7	1157	1	06QAN9
19	194	7.6	659	1	03BA_BACTO
20	193.5	7.6	682	1	03BA_BACTO
21	193	7.5	1229	1	03BA_BACTO
22	193	7.5	1233	1	03BA_BACTO
23	190	7.4	686	2	075Q05
24	189.5	7.4	1220	1	075Q05
25	187	7.3	1156	2	06GUD7
26	186	7.3	1118	2	06GUD7
27	186	7.3	1155	1	06GUD7
28	186	7.3	1155	2	06GUD7
29	186	7.3	1155	2	06GUD7
30	185.5	7.2	719	1	06GUD7
31	184.5	7.2	793	2	06GUD7

32	184.5	7.2	1181	1	03BA_BACTO	003748 bacillus th
33	184	7.2	649	1	03BA_BACTO	045744 bacillus th
34	183.5	7.2	1289	1	05AB_BACUD	045753 bacillus th
35	183	7.1	1118	2	09AM82	09am82 bacillus th
36	183	7.1	1169	2	06BA_BACUR	045705 bacillus th
37	183	7.1	1177	2	06EIX3	06eix3 bacillus th
38	183	7.1	1231	2	06KNV2	06knv2 bacillus th
39	183	7.1	1385	1	05AA_BACUD	045760 bacillus th
40	182.5	7.1	1150	1	09EA_BACTA	09zn19 bacillus th
41	182.5	7.1	1150	2	07IRP4	07irp4 bacillus th
42	182	7.1	1231	1	01BD_BACTZ	09za25 bacillus th
43	181.5	7.1	719	1	01BD_BACTZ	045709 bacillus th
44	180.5	7.1	1167	1	01BD_BACTZ	045709 bacillus th
45	179	7.0	1155	2	093J21	093j21 bacillus th

ALIGNMENTS

RESULT 1	ID	068U02	PRELIMINARY;	PRT;	742 AA.
AC	068U02				
DT	25-OCT-2004	(TREMBLrel. 28, Created)			
DT	25-OCT-2004	(TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004	(TREMBLrel. 28, Last annotation update)			
DE	83-kDa crystal protein.				
GN	Name=Cry31Aa2;				
OS	Bacillus thuringiensis.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1428;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=M15;				
RA	Yung Y.-C., Cote J.-C.;				
RT	"83-KDa crystal protein gene from a novel autoagglutinable, non-				
RT	serotypeable strain of Bacillus thuringiensis."				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY081052; A087458.1;				
DR	InterPro; IPR005639; endotoxin N.				
DR	InterPro; IPR008979; Gal bind like.				
DR	Pfam; PF03945; Endotoxin N; 1.				
DR	SEQUENCE 742 AA; 83104 MW; 4081F7480B0CC134 CRC64;				
SO					
QY	Query Match	100.0%;	Score 2560;	DB 2;	Length 742;
	Best Local Similarity	100.0%;	Pred. No. 7.5e-182;		
	Matches 492;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	IAEPPSTGVITOPRIINDNFPIKYLAKLOFSTNOSDLOPVLTPLRAQACVMMHMLKDA	60		
DB	251	IAEPPSTGVITOPRIINDNFPIKYLAKLOFSTNOSDLOPVLTPLRAQACVMMHMLKDA	310		
QY	61	TTTSGVGOQIDSOQLNGYKALIRLIKVTNDVNTVYNOGLEKAKPLNTSDPEEYLQAG	120		
DB	311	TTTSGVGOQIDSOQLNGYKALIRLIKVTNDVNTVYNOGLEKAKPLNTSDPEEYLQAG	370		
QY	121	RPDISVLRNPFKEVMKNNKVAKYKRGAMGALSTALPPTFGPNYPQALKTVOSSQIFPA	180		
DB	371	RPDISVLRNPFKEVMKNNKVAKYKRGAMGALSTALPPTFGPNYPQALKTVOSSQIFPA	430		
QY	181	PVIGIPGIGITSDSGPFGSGMRPDKTYDDIDLRQLMELIYLOPKSAVFYISDWMKVR	240		
DB	431	PVIGIPGIGITSDSGPFGSGMRPDKTYDDIDLRQLMELIYLOPKSAVFYISDWMKVR	490		
QY	241	ATTVNDYIGRGSNTGAMHMSDPSAITSALGAAGYAPNVVGVVSHSGSYTKGNAP	300		
DB	491	ATTVNDYIGRGSNTGAMHMSDPSAITSALGAAGYAPNVVGVVSHSGSYTKGNAP	550		
QY	301	ANTNAVAPPEFKIPGYLHVSAYGSKAPDADSVNFGFRPVLLSEANOLLDTALQI	360		
DB	551	ANTNAVAPPEFKIPGYLHVSAYGSKAPDADSVNFGFRPVLLSEANOLLDTALQI	610		
QY	361	PATIGITDVVPAFORTBEPINGDALARIMESFSGPFTTVDSPOKOKYIIIRIANNL	420		

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Db 611 PAIGITDVVPAKRTBEPINODAIRINESFTSGGFTTVDSPKOKKIIYRIANML 670
 QY 421 SASTVSLTYNNQTFPTDILNTSLDPNGVRNGSYTLVEGP1IEFSQGTNIFLQSGQKE 480
 Db 671 SASTVSLTYNNQTFPTDILNTSLDPNGVRNGSYTLVEGP1IEFSQGTNIFLQSGQKE 720
 QY 481 FAIDSIIIFSPV 492
 Db 731 FAIDSIIIFSPV 742

RESULT 2

Q9EVR2 PRELIMINARY; PRT; 723 AA.
 AC Q9EVR2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 81-kDa leukemia toxin.
 GN Name=leuk81;
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=84-HS-1-11;
 RX MEDLINE=2034253; PubMed=10882663;
 RA Mizuki E., Park Y.S., Satoh H., Yamashita S., Akao T., Higuchi K.,
 RA Ohba M.;
 RT "Parasporin, a human leukemic cell-recognizing parasporal protein of
 RT Bacillus thuringiensis.";
 RL Clin. Diagn. Lab. Immunol. 7:625-634(2000).
 DR EMBL; AB011065; BAB11757.1.
 DR InterPro; IPR005639; endotoxin N.
 DR InterPro; IPR008979; Gal_bind_like.
 DR Pfam; PF03945; Endotoxin N.1.
 DR PROSITE; PS04521; R1CIN B LECTIN; 1.
 SQ SEQUENCE 723 AA; 81049 MW; 21F873E8286BF52 CRC64;

Query Match 96.6%; Score 2473; DB 2; Length 723;

Best Local Similarity 97.1%; Pred. No. 2.2e-175; Indels 0; Gaps 0;
 Matches 477; Conservative 4; Mismatches 10;

QY 1 IAEPTSTVITQFRILNDFIKYIAKLQSTNQSDLOYVLTLPRAQACVHMLIKDA 60
 Db 232 MAEPSTVITQFRILNDFIKYIAKLQSTNQSDLOYVLTLPRAQACVHMLIKDA 291
 QY 61 TTSVWGQOIDSQOLNGYKAEILRLIKVYTNVNTYNOGLEBKAKPLNYSDEEYDAG 120
 Db 232 TTSVWGQOIDSQOLNGYKAEILRLIKVYTNVNTYNOGLEBKAKPLNYSDEEYDAG 351
 QY 121 RPDIVLSNFKEMKMKVAKYKKGMAISLALPPTPGPNYPKOKLKVVSROIFA 180
 Db 352 RPDIVLSNFKEMKMKVAKYKKGMAISLALPPTPGPNYPKOKLKVVSROIFA 411
 QY 181 PVIGIPGIGTSQDSGPTFGSMRFVYKTYDQIDALQMLYLOPLKSAFYIYSDMKR 240
 Db 412 PVIGIPGIGTSQDSGPTFGSMRFVYKTYDQIDALQMLYLOPLKSAFYIYSDMKR 471
 QY 244 ATTYNDYIGKGSNTGAANHMWSDBSAIYTSALGAAGYAPNVVGRYSHGSGYTKGAP 300
 Db 472 ATTYNDYIGKGSNTGAANHMWSDBSAIYTSALGAAGYAPNVVGRYSHGSGYTKGAP 531
 QY 301 AATNVAAPPEFYKPGYKLSVAYGLSKAPDAADSVWFGFRPYLNEANOLLTDTALQI 360
 Db 532 PNTNVAAPPEFYKPGYKLSVAYGLSKAPDAADSVWFGFRPYLNEANOLLTDTALQI 591
 QY 361 PAIGITDVVPAKRTBEPINODAIRINESFTSGGFTTVDSPKOKKIIYRIANML 420
 Db 592 PAIGITDVVPAKRTBEPINODAIRINESFTSGGFTTVDSPKOKKIIYRIANML 651
 QY 421 SASTVSLTYNNQTFPTDILNTSLDPNGVRNGSYTLVEGP1IEFSQGTNIFLQSGQKE 480

Db 652 SASTVSLTYNNQTFPTDILNTSLDPNGVRNGSYTLVEGP1IEFSQGTNIFLQSGQKE 711
 QY 481 FAIDSIIIFSPV 491
 Db 712 FAIDSIIIFSPV 722

RESULT 3

Q6BE06 PRELIMINARY; PRT; 829 AA.
 AC Q6BE06;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Cancer cell-killing Cry protein.
 GN Name=CryIAD1;
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Al462;
 RA Yamashita S., Satoh H., Katayama H., Akao T., Mizuki E., Park Y.,
 RA Ohba M., Ito A.;
 RT "Cell-killing toxin gene and other genes in 6,698bp DNA from Bacillus
 RT thuringiensis.";
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB116512; BAD35163.1.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin C.
 DR InterPro; IPR005639; endotoxin N.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR008979; R1CIN B lectin.
 DR Pfam; PF03944; Endotoxin C.1.
 DR Pfam; PF03945; Endotoxin N.1.
 DR Pfam; PF03945; Endotoxin N.1.
 DR Pfam; PF00652; R1CIN B LECTIN; 3.
 DR SMART; SM00458; R1CIN B LECTIN; 1.
 DR PROSITE; PS04521; R1CIN B LECTIN; 1.
 SQ SEQUENCE 829 AA; 93841 MW; BBF1F3BEC05F97A3 CRC64;

Query Match 9.5%; Score 244; DB 2; Length 829;

Best Local Similarity 22.2%; Pred. No. 2.6e-09; Indels 152; Gaps 26;
 Matches 128; Conservative 86; Mismatches 210;

QY 9 VITQFRILN---DNFIKIAKLQSTNQSDLOYVLTLPRAQACVHMLIKDAATT--S 63
 Db 164 VLTFRNNGHFNFSMBSFAVNFVN-----LIPYAEANLHLLLRDAVKEGE 214
 QY 64 VMGQOID--SOOLNGYKAEILRLIKVYTNVNTYNOGLEBKAKPLNYSDEEY 116
 Db 215 CMGSTBPGARDMDYR-RLASRTEIYTDHCVTYNOGLEBKAKPLNYSDEEY 273
 QY 117 LQAGRPDISVLRNFKEMKMKVAKYKKGMAISLALPPTPGPNYPKOKLKVVSROIFA 176
 Db 274 NQSGGFSYRAKGEFRTENNNLNYAFRRDWTILVLIIDIAFPPTDGLYSPVSEILR 333
 QY 177 QIPAVVIGIPGIGTSQDSGPTFGSMRFVYKTYDQID--ALRQ-----MELYIQP 224
 Db 334 EYTDIDR-----TWSADANLNTIDALENRNVGSRQOLPTWLTMEKFIYRN 381
 QY 225 LKSAFYIYES-----DKVATYVND-YIGKGSNTGAA-----NH----- 260
 Db 382 TGSITSYHGLMVLGKIRKTNNDQMLPLEGQNTSYTRIDRGEIEGKYVWYARQ 441
 QY 261 -----MW-SSPSAIYTSALGAAGYAPNVVGRYSHGSGYTKGAPANTNVAPE 310
 Db 442 QWETRLQLWNTDVLISLNGVTVGNRWARDVDPYRNIVARSTNNHTEHRLSWIKPE 501

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O| |0 IntelGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq8-seq18-232-723.res made by tport on Thu 27 Oct 105 16:23:23-PST.

Query sequence being compared: US-10-756-778-8 (1-492)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-756-778-8 (1-492) with:
File: rooker778.pep

```

100-
N -
U -
M -
B -
E -
R -
O -
F -
S -
E -
O -
U -
N -
C -
E -
S -
SCORE 0 54 107 161 215 268 322 376 429 483
STDEV

```

PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 492
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 483 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 492
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Sign.	Frame
1. SEQ18-232-723	Sequence 18, Application US/	492	483	484	0.00	0

1. US-10-756-778-8 (1-492)
SEQ18-232-723 Sequence 18, Application US/10756778

Initial Score = 483 Optimized Score = 484 Significance = 0.00
Residue Identity = 96% Matches = 477 Mismatches = 14
Gaps = 0 Conservative Substitutions = 1

```

X 10 20 30 40 50 60 70
IAEPPSTGVITOPRIILNDNFRTYAKLQFSTNOSDLOYPVLTPLRAQACVMHMLLKDATTSVGQOIDSQ
MAEPPSTGVITOPRIILNDNFRTYAKLQFSTNOSDLOYPVLTPLRAQACVMHMLLKDATTSVGQOIDSQ
X 10 20 30 40 50 60 70
QLANGYKAEILRLIKVYNTDVTNTYNOGLEKAKPLNYSDPEEYLQGRPDISVLRNFKEMKMKVAKYK
QLANGYKAEILRLIKVYNTDVTNTYNOGLEKAKPLNYSDPEEYLQGRPDISVLRNFKEMKMKVAKYK
80 90 100 110 120 130 140
RGMMSALSLAALPPTGPNYKQALKVOSROIFAPVIGIPGISTGDSGPFSGMRFPVKTDOIDLARQ
RGMMSALSLAALPPTGPNYKQALKVOSROIFAPVIGIPGISTGDSGPFSGMRFPVKTDOIDLARQ
150 160 170 180 190 200 210
RGMMSALSLAALPPTGPNYKQALKVOSROIFAPVIGIPGISTGDSGPFSGMRFPVKTDOIDLARQ
RGMMSALSLAALPPTGPNYKQALKVOSROIFAPVIGIPGISTGDSGPFSGMRFPVKTDOIDLARQ
220 230 240 250 260 270 280
LMELYIQLKSAFYIYESDMKVATVYNDYIGRGSNTGLAMGMSDDPSVITSLGAGVAPNVGVRY
LMELYIQLKSAFYIYESDMKVATVYNDYIGRGSNTGLAMGMSDDPSVITSLGAGVAPNVGVRY
290 300 310 320 330 340 350 360
SHGGSYTKGMAFPANTNAVAPPEFPGYKLSVSAVGLSKAPDAADSVMGFRVLLLENANQLLTDALOI
SHGGSYTKGMAFPANTNAVAPPEFPGYKLSVSAVGLSKAPDAADSVMGFRVLLLENANQLLTDALOI
370 380 390 400 410 420 430
PAEIGITDVVPAFGRTEEPINGODALIIWESFTSGFPTTVDSPOKOKKIIVRIANNLSASTVSLTYNNO
PAEIGITDVVPAFGRTEEPINGODALIIWESFTSGFPTTVDSPOKOKKIIVRIANNLSASTVSLTYNNO
440 450 460 470 480 490 X
TFEFDIINTSLDPNGVGNAGSYTLVGGPIIEFSQTNIRKLSQKKEFPALDSTIEFSPV
TFEFDIINTSLDPNGVGNAGSYTLVGGPIIEFSQTNIRKLSQKKEFPALDSTIEFSPV
490 500 510 520 530 540
TFEFDIINTSLDPNGVGNAGSYTLVGGPIIEFSQTNIRKLSQKKEFPALDSTIEFSPV
TFEFDIINTSLDPNGVGNAGSYTLVGGPIIEFSQTNIRKLSQKKEFPALDSTIEFSPV

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OM protein - protein search, using sw model

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Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

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SUMMARIES

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3	244	9.5	829	Q68E06	Q68E06 bacillus th
4	230	9.0	825	Q68E09	Q68E09 bacillus th
5	228.5	8.9	1138	Q03749	Q03749 bacillus th
6	225.5	8.8	1138	C7AB_BACTU	Q45707 bacillus th
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8	219.5	8.6	1138	C7AB_BACTU	Q45708 bacillus th
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12	207.5	8.1	1169	C1FB_BACTM	Q66377 bacillus th
13	207.5	8.1	1174	Q45749	Q45749 bacillus th
14	207	8.1	660	Q8R0U6	Q8R0U6 bacillus th
15	200	7.8	1174	C1FA_BACTA	Q03746 bacillus th
16	198	7.7	1154	Q6QAN9	Q6QAN9 bacillus th
17	197	7.7	648	CJAA_BACTU	Q32307 bacillus th
18	196	7.7	1157	C9CA_BACTO	Q45733 bacillus th
19	194	7.6	659	C1BA_BACTO	P17669 bacillus th
20	193.5	7.6	682	CUBA_BACTU	O86170 bacillus th
21	193	7.5	1129	C1BB_BACTU	Q45734 bacillus th
22	193	7.5	1233	C1BC_BACTM	Q45774 bacillus th
23	190	7.4	686	Q75Q05	Q75Q05 bacillus th
24	189.5	7.4	1220	C5AC_BACTU	P56955 bacillus th
25	187	7.3	1156	Q6GU47	Q6GU47 bacillus th
26	186	7.3	1118	Q9AM83	Q9AM83 bacillus th
27	186	7.3	1155	C1AB_BACTK	P06778 bacillus th
28	186	7.3	1155	Q7BE98	Q7BE98 bacillus th
29	186	7.3	1155	Q9F296	Q9F296 bacillus th
30	185.5	7.2	719	C1ID_BACTU	Q9X11 bacillus th
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36	183	7.1	1169	C8BA_BACTK	Q45705 bacillus th
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ALIGNMENTS

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OX	NCBI_TaxID=1428;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=M15;				
RA	Jung Y.-C., Cole J.-C.;				
RT	"83-kDa crystal protein gene from a novel autoagglutinable, non-				
RT	serotypeable strain of Bacillus thuringiensis."				
RL	Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.				
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DR	InterPro; IPR005639; endotoxin N.				
DR	InterPro; IPR008979; Gal_bind-like.				
DR	Pfam; PF03945; Endotoxin N.1.				
SQ	SEQUENCE 742 AA; 83104 MW; 40E1F7480BC134 CRC64;				
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Best Local Similarity	100.0%; Pred. No. 7.5e-182;				
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QY	1	IAEPPSTGVITQFRLINDNFIKYIAKLOFSTNOSDLOYPVLTLPRAQACVGHMLTKDA	60		
DB	251	IAEPPSTGVITQFRLINDNFIKYIAKLOFSTNOSDLOYPVLTLPRAQACVGHMLTKDA	310		
QY	61	TTTSWGQOIDSQINGYAEELIRLIKVTNTDNTTNGLELBRKAPLVSDPEEYLQAG	120		
DB	311	TTTSWGQOIDSQINGYAEELIRLIKVTNTDNTTNGLELBRKAPLVSDPEEYLQAG	370		
QY	121	RPDISVLSNFKYKMKKNAKYKGMAMSLSLAALFPTTGPVNYPKALAVVSGROIFA	180		
DB	371	RPDISVLSNFKYKMKKNAKYKGMAMSLSLAALFPTTGPVNYPKALAVVSGROIFA	430		
QY	181	PVIGIPGSGITSDSGPTFGSRFPVKTVDQIDALROLMEKTIOPKSAVFMYESDMYR	240		
DB	431	PVIGIPGSGITSDSGPTFGSRFPVKTVDQIDALROLMEKTIOPKSAVFMYESDMYR	490		
QY	241	ATVYNDYIGKSGNSGTGAAMHMSDPSALYTSALGAAGYAPNVYGVRSYSGSYTKGNAP	300		
DB	491	ATVYNDYIGKSGNSGTGAAMHMSDPSALYTSALGAAGYAPNVYGVRSYSGSYTKGNAP	550		
QY	301	ANTAAVAFPERKYRGYKIHSAAGLSKAPPAASVYMGFPVLTLENANOLLDTALQI	360		
DB	551	ANTAAVAFPERKYRGYKIHSAAGLSKAPPAASVYMGFPVLTLENANOLLDTALQI	610		
QY	361	PAEIGITDVVPAFGRTPEINGQDAIRIMESFTSGFGFTYVDSPOKOKYIIRIANNL	420		

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Db      611 PAEIGITDVPAFGRTIEEPINGODAIRIWEFTSGGFTYVDSPOKQKXIIYRIANL 670
Qy      421 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPITIEFSQGTNIFKLSQKGE 480
Db      671 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPITIEFSQGTNIFKLSQKGE 730
Qy      481 FAIDSIIFSPV 492
Db      731 FAIDSIIFSPV 742

RESULT 2
Q6EBR2 ID Q6EBR2 PRELIMINARY; PRT; 723 AA.
AC Q6EBR2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 81-kDa leukemia toxin.
GN Name=leuk81;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=84-HS-1-11;
RX MEDLINE=20342553; PubMed=10882663;
RA Mizuki E., Park Y.S., Saitoh H., Yamashita S., Akao T., Higuchi K., Ohba M.;
RT "Parasporin, a human leukemic cell-recognizing parasporal protein of Bacillus thuringiensis.";
RL Clin. Diagn. Lab. Immunol. 7:625-634 (2000).
DR EMBL; AB031065; BAB11757.1; -.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03945; Endotoxin N.1.
DR SMART; PS03945; Endotoxin N.1.
SQ SEQUENCE 723 AA; 81045 MW; 21F873E8286B52 CRC64;

Query Match
Best Local Similarity 96.6%; Score 2473; DB 2; Length 723;
Matches 477; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy      1 IAEPSGTGTTORRIINDPFIKXIAQLQSTNOSDIQYVLTPLPAQACVHMLLKDA 60
Db      232 MAEPSTGVTITOFRIINDPFIKXIAQLQSTNOSDIQYVLTPLPAQACVHMLLKDA 291
Qy      61 TTSVWGQOIDSQOLNGYKAEIRLIRKYVNDVNTYNOGLELEKAKPLVNSDPEETLQNG 120
Db      292 TTSVWGQOIDSQOLNGYKAEIRLIRKYVNDVNTYNOGLELEKAKPLVNSDPEETLQNG 351
Qy      121 RPDISVLRSNFKEVKNKVAKYKGMASALSIALPFTFGPNYKQALKVQSRLPA 180
Db      352 RPDISVLRSNFKEVKNKVAKYKGMASALSIALPFTFGPNYKQALKVQSRLPA 411
Qy      181 PVIIGPGGTTSDSGCTFGSMRPDVKTYYQIDALROLMLYIOPKSAFWIYESDWKR 240
Db      412 PVIIGPGGTTSDSGCTFGSMRPDVKTYYQIDALROLMLYIOPKSAFWIYESDWKR 471
Qy      241 ATTYVNDYIGKRSNTGAAMHMSDPSAITYTSALGAAGYAPNVVGRVSHGGSYTKGMAP 300
Db      472 ATTYVNDYIGKRSNTGLANGMSSDPSVITYSHLAGAGYAPNVVGRVSHGGSYTKGMAP 531
Qy      301 ANTNAVAPPEFKYPGYKLSHVSAYGLSKAPDAADSVMFGRFVLLLEANEQLTDTALQI 360
Db      532 PNTNAVAPPEFKYPGYKLSHVSAYGLSKAPDAADSVMFGRFVLLLEANEQLTDTALQI 591
Qy      361 PAEIGITDVPAFGRTIEEPINGODAIRIWEFTSGGFTYVDSPOKQKXIIYRIANL 420
Db      592 PAEIGITDVPAFGRTIEEPINGODAIRIWEFTSGGFTYVDSPOKQKXIIYRIANL 651
Qy      421 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPITIEFSQGTNIFKLSQKGE 480
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Db      652 SASIVSLTYNNQTFPTDILNTSLDPNGVGNVGSYTLVEGPITIEFSQGTNIFKLSQKGE 711
Qy      481 FAIDSIIFSPV 491
Db      712 FAIDSIIFSPV 722

RESULT 3
Q6EB06 ID Q6EB06 PRELIMINARY; PRT; 829 AA.
AC Q6EB06;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cancer cell-killing Cry protein.
GN Name=cry41ab1;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A1462;
RA Yamashita S., Saitoh H., Katayama H., Akao T., Mizuki E., Park Y., Ohba M., Ito A.;
RT "cell-killing toxin gene and other genes in 6,698bp DNA from Bacillus thuringiensis.";
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB116651; BAD35163.1; -.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin C.
DR InterPro; IPR005639; endotoxin N.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR00772; Ricin B lectin.
DR Pfam; PF03944; Endotoxin C.1.
DR Pfam; PF00555; Endotoxin M.1.
DR Pfam; PF03945; Endotoxin N.1.
DR Pfam; PF00652; Ricin B lectin.3.
DR SMART; SM00458; Ricin.1.
DR PROSITE; PS50231; RICIN_B_LECTIN.1.
SQ SEQUENCE 829 AA; 93861 MW; EBF1F3BEC05F97A3 CRC64;

Query Match
Best Local Similarity 9.5%; Score 244; DB 2; Length 829;
Matches 128; Conservative 86; Mismatches 210; Indels 152; Gaps 26;

Qy      9 VITQFRIIN---DNFIKXIAQLQSTNOSDIQYVLTPLPAQACVHMLLKDA--S 63
Db      164 VLTERRNVNGHFRENSMPSFAVNFENV-----LPLVAEAEANLHLLLRDAVKEGE 214
Qy      64 VMGQOIDSQOLNGYKAEIRLIRKYVNDVNTYNOGLELEKAKPLVNSDPE-----EY 116
Db      215 GMGSTDPGAEKDDMYR-RLRSRTETLYDHCVTNTYNOGLEQAKSLQANVSYSRYEWTQY 273
Qy      117 LQAGRPDISVLRSNFKEVKNKVAKYKGMASALSIALPFTFGPNYKQALKVQSRLPA 176
Db      274 NQSGGFSYREAKGEYREKEMNNLVNAPRRDITLVLIDIAQPTYPDPGLYRPAVKSLETR 333
Qy      177 QIPAVVIGIPGGLTSDSGCTFGSMRPDVKTYYQID---ALRQI-----MELYIQP 224
Db      334 EYVYTDIRG-----TTWSDANLITIDAIENMVGSRQQLFTWLTMEKFIYRN 381
Qy      225 LKSAFWIYES-----DMKVAATYVND-YIGKRSNTGA-----MH----- 260
Db      382 TGSITSYTHGDMNGLEKIKRTNDNDQWLPLEQNTSYTRIIRDPGIELGNVWYVYATQ 441
Qy      261 -----MW-SSDPSAITYTSALGAAGYAPNVVGRVSHGGSYTKGMAPANTNAVAPPE 310
Db      442 QMFETRLQLQVNTDVLSLNGVYGNEFWADVDVPRNRIYARSTRNHIEHRLSWIKFE 501
```


QY 311 -----FKYPGYKLHSVSAVGLSKAPDAADSVMEGFRPVLLNEANQLLTDALQIPAE 363
Db 502 PVRNCPFAMPGYQLSALLFGWTH-----NSV-----DPENFIASDRITQIPAV 546
QY 364 IGI-----TDVPAFGRTPEEPINGODAIRI-----WESFTSGFGFTYVDSPOKOKYKI 412
Db 547 KGYLVNCGATVVRGSGNT-----GGDLVLPAYNQQTQLRVKVPSTTA---RTRGYNV 598
QY 413 IYRANNLSAS-----TVSLTYN-----NOFFFDIANTSLDPNGVAGNYSYTLV 458
Db 599 RIRVASEBNANLFWGKYVDYTNRFETIGNVAVNQTFSGSM-----TNSFKYL 646
QY 459 EGPILFESQGTNIFKLQ---SQKGEFAIDSIIFSPV 491
Db 647 DA--IGFAANEERIEIRKCSGGRPIYIDKIEFTIV 680

RESULT 4
O6BE09 PRELIMINARY; PRT; 825 AA.
AC O6BE09, 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Cancer cell-killing Cry protein parasporin-3.
GN Name=CRY41Aa1;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A1462;
RA Yamashita S., Saitoh H., Katayama H., Akao T., Mizuki E., Park Y.,
RA Ohba M., Ito A.;
RT "cell-killing toxin gene and other genes in 8,605bp DNA from Bacillus
thuringiensis.";
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A1462;
RA Yamashita S., Saitoh H., Katayama H., Akao T., Mizuki E., Park Y.,
RA Ohba M., Ito A.;
RT "cell-killing toxin gene and other genes in 8,572bp DNA fragment from
Bacillus thuringiensis.";
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB116650; BAD35160.1; -
DR EMBL; AB116649; BAD35157.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0015288; F:protein activity; IEA.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defence response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR008997; RicinB_like.
DR InterPro; IPR00772; RicinB_lectin.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF03945; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_N_1.
DR Pfam; PF00652; Ricin_B_lectin; 3.
DR SMART; SM00458; RICIN_1.
DR PROSITE; PS02031; RICIN_B_LECTIN; 1.
KM Porin.
SQ SEQUENCE 825 AA; 93693 MW; 98C4CSBAFF996B2 CRC64;

Query Match 9.0%; Score 230; DB 2; Length 825;
Best Local Similarity 21.0%; Pred. No. 2.8e-08;
Matches 120; Conservative 90; Mismatches 213; Indels 148; Gaps 24;

QY 9 VITGRINL---DNFIKTIKAKLQFSTNQSDLQYPVLTLPRLRAQACVMMHMLLKDAAT--S 63

Db 164 VLTEFRVNVNGHFENSMSPFAVRNEVN-----LLPYAEKANIHLILRLDAVKGGE 214
QY 64 VWGQID--SQQNGVYAEELIRLIKVTNDVNTTYNGCLEKAKPLNYSPE-----EY 116
Db 215 GWGMSITPGARDWDR-RLRSTRETYDHCVTNYNGQLQOAKSLQANVSYSYSPWTQY 273
QY 117 LQAGRDISVLRNSFKEMKKNKAKYKGMASALSIALFPTEGPNPKQALKVQSR 176
Db 274 NQSGFSYREAKGKYRTETNNMLNAPRRMTLIVLDIIQFPYDGLVSRPKSELTR 333
QY 177 QIFAPVIGIFGGLTSGDSGPFSGMRPDVXTYDID--ALROL-----MELYIQP 224
Db 334 EYVTDING-----TWRS DANLNTIDAIEHRMVGSRQLQFTWLTEMKFYIRN 381
QY 225 LKSAFYWYES-----DMKRAITYND-YIGKGSNTGAA-----WH----- 260
Db 382 TGSITSYTHDDLWGLKERTKRTNDNDQWLPLEGQNTSYTRIDRPGIELGNVYVARTQ 441
QY 261 -----MW-SSDPATYTSALGAGYAPNVVGVSHSGSYTKGMAPANTVAVAPFE 310
Db 442 QMFETRLQLMANTDUSLNAAGVGNFWRDVPDYNTIYARSTRNFIENHRLSMWKE 501
QY 311 -----FKYPGYKLHSVSAVGLSKAPDAADSVMEGFRPVLLNEANQLLTDALQIPA- 362
Db 502 PVRNCPFAMPGYQLSALLFGWTHNSVDLNNISQYR-----ITQIPAV 546
QY 363 -----EIGITDVPAFGRTPEEPINGODAIRIWESTSGFGFTYVDSPOKOKYKIYRIAN 418
Db 547 KAYWNRGAFSVIRPGST-----GGLVOL-----GTGEVSVKVPEDQSDWYVRI 595
QY 419 NLSAST-----VSLTYN--NOFFFDIANTSLDPNGVRNGVSYTLVEGPIL 463
Db 596 RYAGSGRGLNVKKYVSIHASTYTDYNTM-----SSSTQGTYSFOYLD--VY 643
QY 464 EFSQGTNIFKL---GSQKGEFAIDSIIFSPV 491
Db 644 NFRLAPEPEFVWLTMESGPIWIDKIEFTIV 674

RESULT 5
C7AA_BACTU STANDARD; PRT; 1138 AA.
ID C7AA_BACTU 30-MAY-2000 (Rel. 39, Created)
AC 003749;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Pepticidal crystal protein cry7Aa (Insecticidal delta-endotoxin
DE CRYVITA(a) (Crystalline entomocidal protoxin) (129 kDa crystal
protein).
GN Name=CRY7Aa; Synonyms=CRYIIC, CRYVITA(a);
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92384571; PubMed=1514800;
RA Lambert B., Hofte H., Anny K., Jansens S., Soetaert P., Peferoen M.;
RT "Novel Bacillus thuringiensis insecticidal crystal protein with a
RT silent activity against coleopteran larvae.";
RL Appl. Environ. Microbiol. 58:2536-2542(1992).
CC -I- FUNCTION: Promotes colloid-osmotic lysis by binding to the midgut
epithelial cells of Coleoptera. This protein is not toxic in its
natural form. It is highly toxic to Colorado potato beetle larvae
after an in vitro solubilization and trypsin activation step.
CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.
CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -I- SIMILARITY: Belongs to the delta endotoxin family.
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; M64478; AAA22351.1; -;
 DR EMBL; A07236; CAA00646.1; -;
 DR PIR; A48944; A48944.
 DR HSSP; P07130; 1DLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin.C.
 DR InterPro; IPR008979; endotoxin_N.
 DR InterPro; IPR008979; Gal_bind_like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 DR Sporulation; Toxin.
 KW SEQUENCE 1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;
 SQ

Query Match 8.9%; Score 228.5; DB 1; Length 1138;
 Best Local Similarity 22.4%; Pred. No. 5.7e-08;
 Matches 124; Conservative 70; Mismatches 216; Indels 143; Gaps 23;

QY 9 VTGRIPLNDNFIKYIAKQFSTNOSDQ-YPVLTPLRAQACMHLMLKDATT--SVW 65
 DB 157 VATEFPIIDSLF-----EFSWPFKVTGYEIPILTVAQAANHLALRDSITLYGDKW 209
 QY 66 G--QQIDSOQLNGYKAEILRLIKVYNDVNTVYNOGLEBKAKPLNYSDEEYLQAGR 123
 DB 210 GTTQNNIENYNRK---KRISYSDHCKTKWNSGLS----- 243
 QY 124 ISVLSNFKKWKVKNKAKYKRGMAALSALAFPTFGPNYKQALKVQSRQIFAPVY 183
 DB 244 ----RANGSTYEQWIVNFRREMILMALDIVAFPHDPRKXSMETSTQTLREVTDPV 299
 QY 184 GIPGGITSDSGPTFGSM-RFDVKTYDQIDALRQMLELYIQPLKAYFVIYESDKVRRAT 242
 DB 300 SL--SISNPDIGPSFQMENTAIRPHLVYDEL-----YIYTSKYKAFSH 344
 QY 243 YVNDYIGKRGSTGAMHMS-----SDPSAIYTSAL--GAAGYAPNVGVRSHG 292
 DB 345 EIQPD-----FYSAHKVFSKSEBSNLTYTGIGKTSYISS--GAVSEHN 391
 QY 293 SYTKGAPANTNAYAFPEFKYP---GYKLHSVAVGL-----SKAPDAADSVW 337
 DB 392 DLYRTLA-----APSVVVPYTONYGVEFYGKGVHNRGDKXYDLVYDSIDLP 444
 QY 338 FGFRPVLEANEANQLITPAQIPAEIGITDVVPAFGTE-----EPINGQDAI 386
 DB 445 PDGEPI-HEKYTHRLCHATAIFKSTPDYDNATPIFSWTHRSLEYNRIYPMKTIKIPAV 503
 QY 387 RIWE-----SPTSGEFT-----YTVDSPOKOKKIIYRIANNLSAST 424
 DB 504 KMYKLDDBSTVVKVGFEGDLYKRGSTGYIGDIAKTVNSPLSKRVAVRATVNSGQF 563
 QY 425 VSLTVNNQTFPTDILNT-SLDPNVGRGNYSYTLVE-GRIFESQGTNIFKLG---SOK 478
 DB 564 NYIYNDKILQTKFQNTVETIGEGKDLTYGSGFYIYESTTIGRPDRHKITLHLSLNN 623
 QY 479 GEPALDSIIFSPV 491
 DB 624 SSFYVDSIEFIPV 636

RESULT 6
 C7AB_BACUA STANDARD; PRT; 1138 AA.
 ID C7AB_BACUA
 AC Q45707;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Pesticidal crystal protein cry7Ab (insecticidal delta-endotoxin
 DE CryVIIa(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
 DE protein).
 GN Name=cry7Ab; Synonyms=cryVIIa(b);
 OS Bacillus thuringiensis (subsp. dakota).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OK NCBI_TaxId=132268;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD511;
 RA Payne J.M., Fu J.M.;
 RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
 RT coleopteran-active toxins."; 15-FEB-1994.
 RL Patent number US5286486; 15-FEB-1994.
 CC -1- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
 CC epithelial cells of Coleoptera.
 CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -1- SIMILARITY: Belongs to the delta endotoxin family.
 CC -----
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 CC or send an email to license@isb-sib.ch).

DR EMBL; U04367; AAA21120.1; -;
 DR HSSP; P07130; 1DLC.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin.C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal_bind_like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 DR Sporulation; Toxin.
 KW SEQUENCE 1138 AA; 129778 MW; 01DF7072C074CE88 CRC64;
 SQ

Query Match 8.8%; Score 225.5; DB 1; Length 1138;
 Best Local Similarity 22.5%; Pred. No. 9.5e-08;
 Matches 126; Conservative 75; Mismatches 207; Indels 151; Gaps 25;

QY 7 TGVINQFPLNDNFIKYIAKQFSTNOSDQYPVLTPLRAQACMHLMLKDATT--SV 64
 DB 155 TRVIDRFPLIDALFESYMPFRVA-----GEIPLTLVYAQAANHLALRDSITLYGDK 208
 QY 65 WG--QQIDSOQLNGYKAEILRLIKVYNDVNTVYNOGLEBKAKPLNYSDEEYLQAGR 122
 DB 209 MGFQNNIENYNRK---KHISYSHCKWKWNSGLS----- 243
 QY 123 ISVLSNFKKWKVKNKAKYKRGMAALSALAFPTFGPNYKQALKVQSRQIFAPV 182
 DB 244 ----RANGSTYEQWIVNFRREMILMWLIDIAAFPIYDPRMYSMETSTQTLREVTDP 298
 QY 183 IGIPIGITSOSGPTFGSMRFDV-KTYDQIDALRQMLELYIQPLK-----SAFW 231
 DB 299 ISL--SISNPDIGPSFQMENTAFTPLVD--YLDLTYTYSKYKAFSHEIOPDLFW 353
 QY 232 -IYESDMKVRATYVNDYIGKRGSTGAMHMSDPSAIYTSAL--GAAGYAPNVGVRY 288
 DB 354 CVHKVSKF-----KSFQSNLYTTGIGYKTSY---ISSGAY 386
 QY 289 SHGS--YTKGMAPA-----NTNAYAFPEFKYPGYKLH---SVSAYGLSKAPDAADSVW 337
 DB 387 SFRGNDIYRTLAAPSVVVPYTONYGVEFYGKGVHNRGDKXYDLTY--DSIDLP 444
 QY 338 FGFRPVLEANEANQLITPAQIPAEIGITDVVPAFGTE-----EPINGQDAI 386

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Db 445 PDGEP1-HEKXTHRLCHATAISKSTPDYDNTATIPFSWTHRSABEYNNRIYENKIKIPAV 503
Qy 387 RIWE-----SFTSGGFT-----YTVDSPQOKOKYKIRIANNLSA-- 422
Db 504 KMYKLDLSTVVKPGPGFTGDLVKRGSNGYIGDIKATVNSPLSKTRVRVATASVSLF 563
Qy 423 -----STVSLTYNNQTFPTDILNTSLDPNGVNGVSYTLVE-GRIIEFSGGTNIFKLG- 475
Db 564 NVFINDLALQKNQSTVETI-----GEGDLTFYGSNGYIEYSTTICFPHEHPRTIHL 617
Qy 476 ---SOKGEFALDSIFSPV 491
Db 618 NHTSNNSPFYVDYSIEFIPV 636

RESULT 7
C9DA_BACTP STANDARD; PRT; 1169 AA.
ID C9DA_BACTP
AC 006014;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Peptidicidal crystal protein cry9da (insecticidal delta-endotoxin
DE CryIXD(a)) (Crystalline entomocidal protoxin) (132 kDa crystal
DE protein).
GN Name=cry9da; Synonyms=cryIXD(a);
OS Bacillus thuringiensis (subsp. japonensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=128936;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N141;
RA Asano S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of insects.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D85560; BAA19948.1; -
CC DR HSSP; P07130; 1DLC.
CC DR InterPro; IPR001178; Endotoxin.
CC DR InterPro; IPR005638; endotoxin_C.
CC DR InterPro; IPR005639; endotoxin_N.
CC DR InterPro; IPR008979; Gal_bind_like.
CC DR Pfam; PF03944; Endotoxin_C_1.
CC DR Pfam; PF00555; Endotoxin_M_1.
CC DR Pfam; PF03945; Endotoxin_N_1.
CC DR Sporulation; Toxin.
CC KW SEQUENCE 1169 AA; 132228 MW; 659AB257229D5E59 CRC64;

Query Match 8.7%; Score 223.5; DB 1; Length 1169;
Best Local Similarity 22.3%; Pred. No. 1.4e-07;
Matches 130; Conservative 78; Mismatches 192; Indels 183; Gaps 30;

Qy 9 VITOPRIINDNPRIKXIAKQSTNGSDQYVPLTPLAQAQCVHMLKXATT--SVWG 66
Db 168 VSGRNILDSLFTQMP--SFGSGSGSYNTATILLPVAQAANHLHLKADHDYGAAG 225
Qy 67 QOIDSQQLNGYKAEILRIKVTYNDVNTYNGLELEKAKPLANSYDPEYLAQGRDISV 126

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Db 226 --LNQTOIDQFHSRQSLTQTYNNHCVTAYNDL-----AE 259
Qy 127 LRSNFEKWMKKNKAYKXRGAMASALSLALFPTEGNYPRKQALKVQSRQIFAPVIGI - 185
Db 260 LRGTAL--SNFKTNQRRKRETLTAMDVLALFPYINLRQYPRDGNRPDLTHEVYDPAFD 317
Qy 186 ---PGITSQ-----DSGPTF-GSMRFV-----KTYQDIALROLMELYIQPLK 226
Db 318 PLEGP---TQLCRSWYINPAFRHNLNFSVLENSLIRPHLPBELSNQLIVN--YQNG 372
Qy 227 SA-----YFWIYESMKRA--TYVNDYIGKR-----GNTGQAMH 260
Db 373 SAMRGSRRVRYHHSIIQKRSYGLSDPVGANINQNDIYQIISQVSNFASVSGSYS 432
Qy 261 MMSDSPAIYTSA---LGAAGYAPNVGV-----RSHGGSY 294
Db 433 VMDTN---FYLSQGVSGISGYTQGIIPAVCLQGRNSTDELPSINPBGDIIRYSHLSH 489
Qy 295 -----TKMAPANTNAYAPPEFKYPGYKLSVSAYGLSKAPDAADSVMGFRPVLL 346
Db 490 ITQYRFQATQSGSPSTVSANLP-----TCVWTRHDVLD 523
Qy 347 N--BANGLLDTALQIP-----AEIGITDVV-PAFGRTEBPINGQALRWESFTSGFG 397
Db 524 NTRIANQI-----TQLPLVAYELSGATVWKGGF-----TGGDVIR--RNTGGFG 569
Qy 398 -FTTVSPQOKOKYKIRIYRIANNLSAS---TVSLTYNNQTFPTDILNTSLDPNGVRNGY 453
Db 570 AIRVSTGPILTQRRIRFRTASTIDPDPFVYRGCTITNNRFRKTMN-----RQESRYE 624
Qy 454 SYTLVEGPI-IEFSGTNIFPLGSO---KGEFALDSIFSPV 491
Db 625 SYRVEFTTPNFTQSDIIRTSIQSGNGEYVLDRIEIPV 667

RESULT 8
C7AB_BACUK STANDARD; PRT; 1138 AA.
ID C7AB_BACUK
AC Q45708;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Peptidicidal crystal protein cry7ab (insecticidal delta-endotoxin
DE CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
DE protein).
GN Name=cry7ab; Synonyms=cryVIIA(b);
OS Bacillus thuringiensis (subsp. kumamotoensis).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=132267;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD867;
RA Payne J.M.; Fu J.M.;
RT "Coleopteran-active Bacillus thuringiensis isolates and genes encoding
RT coleopteran-active toxins.";
RL Patent number US526486, 15-FEB-1994.
CC -1- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
CC epithelial cells of Coleoptera.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC -----

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DR EMBL: U04368; AAA21121.1; -.
DR HSSP; P07130; 1DLC.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
DR Sporulation; Toxin.
KW SEQUENCE 1138 AA; 129658 MW; E12DC80C0A56D1DA CRC64;
SQ
Query Match      8.6%; Score 219.5; DB 1; Length 1138;
Best Local Similarity 22.2%; Pred. No. 2.6e-07;
Matches 123; Conservative 75; Mismatches 215; Indels 141; Gaps 23;
QY 7 TGVITQFRILNDNFYKIAKLFSTNQSDLYQYVLTLPRAQAQVWHMLMLDATTSSVWG 66
DB 155 TVIDRFRLDALFESYMSFRVA-----GYEIPLTIVYAQAANHLALDST--LYG 206
QY 67 QOIDSQQLN--GYKAEILRLIKVTNDVNTTYNOGLELEKAKPLNYSDEEYLQAGRPD 123
DB 207 DKMEFTQNNIEENYKQK-KHISEYSNHCWKWYNSGLS----- 243
QY 124 ISVLSPFEKWKMKVAKYKRGMAASALSLAAPTPEGPNYPKQALKVYQSRQIFAPVI 183
DB 244 ----RUNGSTYQWIMYNFRREMILMDLDIAVFIYDPRMYSMETSTQLTREYTDPI 299
QY 184 GIPGIGTSDSGPTTFGSM-RFDVKTYDQIDALROLMELYIOPLKSAFYWIESDWKVRAT 242
DB 300 SL--SISNCGIGPSPSQMENTAIRPHLVDYDEL-----YIYSKKYKAFSH 344
QY 243 YVNDYIGKRGSTGAAHMKWS-----SDPSAIYTSAL--GAAGYAPNVGVKRYSHCG 292
DB 345 EIQPLD-----FYMSAHKVSFKQSEQSNLYTTGITYKTSGLYS-----G 384
QY 293 STT-KGMAPANTNAVAPFEKYP--GYKLHSVSAVGL-----SKAPDAADV 336
DB 385 AISFGKNDIYRFLA-APSVVVPYTONYGEVEEFGVAGHYVRGDKYDLTYSDIDL 443
QY 337 MGFPRVLLLENANQLITDTALQIPAEIGITPVVPAFGRT-----EPINGQDA 385
DB 444 PDDGEPI-HEKYTHRLCHATAISKSPVDNATIPFFSWTHRSABEYNNIYNNKTIKIPA 502
QY 386 IRIWE----SFTSGEGFT-----YTVDSPOKQKIKIYRIANNLSAS 423
DB 503 YMYKYLGDSTYVKGSGFTGDLVKKGSNGYIGDIKATVNSPLSQYRVAVYATVNSQ 562
QY 424 TVSLTYNNQTFPTDIINT-SLDPNGVRNGYGSYTLVE-CPILIEFGQNTIIFLGS----SQ 477
DB 563 FNVYINDKITLQRFQNTVETTGEGKDLTYGSGYIEYSTTIQFPDKHPKITLHLSLSN 622
QY 478 KGEFAIDSIIFSPV 491
DB 623 NSSFYVDSIEFIPV 636
RESULT 9
ID Q9S603 PRELIMINARY; PRT; 645 AA.
AC Q9S603;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Delta-endotoxin (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=searovar japonensis type;
RX MEDLINE=99025985; PubMed=9806979;
RA Masano N., Ohba M.,
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RT "Assignment of delta-endotoxin genes of the four lepidoptera-specific
RT Bacillus thuringiensis strains that produce spherical parasporal
RT Inclusions.";
RT Curr. Microbiol. 37:408-411 (1998) .
DR EMBL; AF042733; AAB97923.1; -.
DR HSSP; P07130; 1DLC.
DR GO; GO:0005102; F:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind_like.
DR Pfam; PF03944; Endotoxin_C; 1.
DR Pfam; PF00555; Endotoxin_M; 1.
DR Pfam; PF03945; Endotoxin_N; 1.
FT NON TER 1 645
SQ SEQUENCE 645 AA; 72967 MW; 143E5132B890CE3 CRC64;
Query Match      8.4%; Score 214.5; DB 2; Length 645;
Best Local Similarity 22.0%; Pred. No. 2.9e-07;
Matches 127; Conservative 78; Mismatches 188; Indels 183; Gaps 30;
QY 9 VITQFRILNDNFYKIAKLFSTNQSDLYQYVLTLPRAQAQVWHMLMLKDATT--SVWG 66
DB 153 VSQRNLDLSLFTQPM--SFGSGPSONVATITLIPYAQAANHLALDKADIDYGAWG 210
QY 67 QOIDSQQLNGYKAEILRLIKVTNDVNTTYNOGLELEKAKPLNYSDEEYLQAGRPDISV 126
DB 211 --LNGTQIDQGHRSRQSLTQYTNHCVTAYNDGL-----AE 244
QY 127 LRSNFEKWKMKVAKYKRGMAASALSLAAPTPEGPNYPKQALKVYQSRQIFAPVIGI- 185
DB 245 LRGITAE--SWFKVQYRREMTLTAMDVLVAFPPYNNLRQYPDGPNQLTREYTDPIAFD 302
QY 186 ----PGITSQ-----DSGPTF-GSMRPDY-----KTYDQIDALROLMELYIOPLK 226
DB 303 PLEQP--TTQCRSWYINPAPRNHLNPSVLENSLIRPHILFERLSNQLILVN--YQNG 357
QY 227 SA-----YWIYEDSKVRA--TYVNDYIGK-----GSNITGAAMH 260
DB 358 SAMRGSRRRYHLYHSIIQEKSYGLSDPVGANINVNQNDIYQIISQVSNFASPVGSSYS 417
QY 261 MMSDPSAIYTSA--LGAAGYAPNVGV-----RISHGSY 294
DB 418 VMDTN---FYLSGQVSGISGVTQGGIPAVCLQQRNSTDELPSLNEGGDIIRNYSRLSH 474
QY 295 -----TKMAPANTNAVAPFEKYPGYKLHSVSAAGLSKAPDAADVWFGPRVILE 346
DB 475 ITQYRFQATQSGSPSTVANLP-----TCWTHRDVDLD 508
QY 347 N--EAMQLITDTALQIP-----AEIGITDVV-PAFGTEEPINGQDAIRIWESFTSGFG 397
DB 509 NITANQI-----QLPLVAKAYELSSGATVVKGPGF-----TGGDVIR--RTMTGFG 554
QY 398 -FTYVDSPOKQKIKIYRIANNLSAS--TVSLTYNNQTFPTDIINTSLDPNGVRNGY 453
DB 555 AIRVSVTGPLTQRYAIRFRVASTIDFDFVTRGGTTINNFRFTYMN-----RQGSRYE 609
QY 454 SYTLVEGPI-IEFGQNTIIFLGSQ----KGEPAID 484
DB 610 SYRIVEFTTPNFQSDIIRTSIQGSGNGEAVYID 645
RESULT 10
ID Q6BE03 PRELIMINARY; PRT; 810 AA.
AC Q6BE03;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Cry protein.
```

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GN Name=cry42Aa1;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AL62;
RA Yamashita S., Saitoh H., Katayama H., Akao T., Mizuki E., Park Y.,
RT "cell-killing toxin gene and other genes in 4,567bp DNA from Bacillus
RT thuringiensis."
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL; AB116652; BAD3166.1; -
DR GO; GO:0005102; P:receptor binding; IEA.
DR GO; GO:0006952; P:defense response; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005639; endotoxin.C.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR008979; RicinB like.
DR InterPro; IPR00772; Ricin_B_lectin.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_M_1.
DR Pfam; PF00652; Ricin_B_lectin; 3.
DR SMART; SM00458; RICIN_1.
DR PROSITE; PS50231; RICIN_B_LECTIN; 1.
SQ SEQUENCE 810 AA; 91300 MW; 61D27179220D249B CRC64;

Query Match 8.3%; Score 211.5; DB 2; Length 810;
Best Local Similarity 23.3%; Pred. No. 6,6e-07;
Matches 133; Conservative 81; Mismatches 210; Indels 147; Gaps 29;

QY 2 AEPSTGVITQRIINDNFIXIAKLQSTNSDLOYPVLTPLRAQACWMLMLKDAT 61
DB 158 SEPIQRLQSLQPTANTPTFIVGSMSLFRVGRH---EVLPLT--TFVQANHLHLRLDAI 211
QY 62 T--SWGQQLDSQQLNGYKAEILIRIKYITNDVNTTNGGLEAKPLANSDPREYQA 119
DB 212 MFGESWG--MCPVTVAGYQNDNFNNRIADYTVSVINQGLQKATTLTANLRDEKYYWA 269
QY 120 GRPDISV-LRSNFKVEMKNNKAKYKRGMAASLSLALFPFGNRYKQALKVQSRQI 178
DB 270 RYVNSVPEPAPYAGMENWNNLYNNRRDMLTVALVLPPTYNDQYPIAPKIQITKEI 329
QY 179 FAPVIGIPGIGTSDGCPFGSMRPDVKYDQIDALROLMELYIQPLSAAYFWIYESD-- 236
DB 330 YTELKGNMGN-TKRS-----MDAIDA-----ELI--PPRLFTWLESVDMH 368
QY 237 -WKVRA-----TYVDYIGKRGSTGAAMHMSDPSALYTSALGAAGYAPNVV----- 284
DB 369 RWPISAGYVYTFQNAIGIKHR-----YKTTLSQTLTSLRGASGNFNLVPAERTI 420
QY 285 -GVRSHG-GSYT-----KGNAP-----ANTNAVAPF-----EKYKGYVLT-- 319
DB 421 NKVQNHQBGLTFPSFRRSGSDPLNLGITADKPKYVSTWARI PVESGDTQANHLRSLWT 480
QY 320 -----SVSAYGLSKAPDAADSVMFGRFVLLNEANQLTDLTALQIPAEIGI-----T 367
DB 461 GNVITDELSTPARG-HYNPTIYISCAEGWTHLSVE-RSNEIKSDKITQIPAYVAPQLSNN 538
QY 368 DVPAFGRTPEPINOQDAIRIWESFTSGFGFTY-----YDSFKQKYYKIIYRIANL- 420
DB 539 SVVRGPGST-----GGDLVQ--FSATSSGNKQLMIKVKPTTIALGRFPKRIRYAAAVNT 592
QY 421 -----SASTVSLTVN-----NOTFFDILNTSLDNGVYRGVNGSYTLVWG 460
DB 593 FTVQACVTGVACWETATKSVITTYSGTLTYNAFKYVDIFE-----IPANSEPSL--- 642
QY 461 PLIEFSOGTNIPIKLGSKGKEPAIDSIIPSPV 491
DB 643 ---EF-----LSTSGGPYIYIDKIEFIIV 662

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RESULT 11
C1A_BACTU
ID C1A_BACTU STANDARD; PRT; 1167 AA.
AC Q45738;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIa (Insecticidal delta-endotoxin
DE CryI(a)) (Crystalline entomocidal protoxin) (133 kDa crystal protein).
OS Name=cryIa; Synonyms=cryET4, cryI(a);
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL B-21110 / EG5847;
RA Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
RT "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
RT toxic to lepidopteran insects."
RL Patent number US5322687, 21-JUN-1994.
CC -1- FUNCTION: Promotes colloidomotic lysis by binding to the midgut
CC epithelial cells of many lepidopteran larvae.
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during
CC sporulation and is accumulated both as an inclusion and as part of
CC the spore coat.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-
CC terminus.
CC -1- SIMILARITY: Belongs to the delta endotoxin family.
CC -----
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CC -----
DR EMBL; L32019; AAA2241.1; -.
DR HSSP; P02965; IC1Y.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin.C.
DR InterPro; IPR005639; endotoxin.N.
DR InterPro; IPR008979; Gal_bind_like.
DR Pfam; PF03944; Endotoxin_C_1.
DR Pfam; PF00555; Endotoxin_M_1.
DR Pfam; PF03945; Endotoxin_M_1.
KW Sporulation; Toxin.
SQ SEQUENCE 1167 AA; 132760 MW; 3B7357D14E655FC7 CRC64;

Query Match 8.2%; Score 210.5; DB 1; Length 1167;
Best Local Similarity 21.9%; Pred. No. 1.3e-06;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

QY 3 EPPSTGVITQRIINDNFIXIAKLQSTNSDLOYPVLTPLRAQACWMLMLKDAT 62
DB 123 EAKSRVYDRRIIDGLIENIPSPRI-----IGFVPLLSVYVQANHLALRDSV- 175
QY 63 SWGQQLDSQQLNGYKAEILIRIKYITNDVNTTNGGLEAKPLANSDPREYQAQ 120
DB 176 -IFGRMGLTTKNVNDIYNROI REIHEYSNHCVDYTNTELE----- 215
QY 121 RPDISVLRSNFKVEMKNNKAKYKRGMAASLSLALFPPTGPN-YPKQALKVQSRQIF 179
DB 216 -----RLGFRSLAQWRIVYQFRRELTLTVLIDVALLFPNYSRLYPTQTSQTLREIVT 268
QY 180 APVIGIPGIGTSDGCPFGSMRPDVKYDQIDALRLQ-----NELYIQPLSAAYFW--- 231
DB 269 SPVSEPFYGVV--NSGNITGL-----TEQDIRPHLMDPNSMIMTISDNKRREHYMSGL 321
QY 232 --LY-----ESDWKVRATVYND-----YIGKR 251

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DB 322 EMTAVFTGFAQVFPPLVGTGEGSAPPLITVASVNDGIYRIILSAPFYSAFLGTVLGSR 381
QY 252 GSNTGAAMHMMSSDPSAIYTSALGAGYAPNVGVRYSHSGSYTKGMAPANTNAYAPPEF 311
DB 382 GEKFPDFALNNISPPSTIYR---PGTVDSLVI-----PQONSVP--- 421
QY 312 KYPGYKLSVSAVYGSKAPDADSVMEFG--RPVLIENANQLDITLQIAEIGTIDV 369
DB 422 -----HRGSSHRISHVTMRASSPFLMWHRSATTTNTIN--PNAIIQIP-----L 464
QY 370 VPAFGRTEEPINGODAIRIMESFTSGFGFT-----YTVDSPQOKYKI 412
DB 465 VMAFPLH-----SGATVVR-----GPGTTGGDILRRITNTGPFADMVNIITGELSQRKV 513
QY 413 IYRIANNLSASTVSLTYNNQTFETDILNTSLDPNGVGNVGSYTLVEGPIL----- 464
DB 514 RIRY-----ASTTDL-----QFTTRINGTSVN-----QGNF--QRTMNRGDNLESNGNFRTAG 558
QY 465 -----FSGGTNIFKLGSQ---KGEFADSIIFSP 490
DB 559 FSTPFSFNAOSTFTLTGTQAFSNOEYVIDRIEFVP 593

RESULT 12

CIFB_BACTM

ID_CIFB_BACTM STANDARD; PRT; 1169 AA.

AC 066377; Q9RC19;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pesticidal crystal protein cryIpb (Insecticidal delta-endotoxin
cryIpb(b)) (Crystalline entomocidal protoxin) (132 kDa crystal protein).
GN Bacillus thuringiensis (subsp. morrisoni).
OS Bacillus thuringiensis (subsp. morrisoni).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NC NCB1_TaxID=1441;
RN [1]
RP SEQUENCE FROM N.A.
RA Song F., Zhang Z., Ding Z., Chen Z., Li G., Huang D.;
RT "A novel cryIpb gene from Bacillus thuringiensis subsp. morrisoni";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=INA67;
RA Maenuda K., Asano S.;
RL Submitted (Mar-1998) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Promotes colloidotomotic lysis by binding to the midgut
epithelial cells of insects.
CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
the spore coat.

CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
terminus.
CC -!- SIMILARITY: Belongs to the delta endotoxin family.

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CC or send an email to license@sib-sib.ch).

CC EMBL; AF062350; AAF21767.1; -;
DR EMBL; AB012288; BAA25298.1; -;
DR HSSP; P02965; 1CTY.
DR InterPro; IPR001178; Endotoxin.
DR InterPro; IPR005638; endotoxin_C.
DR InterPro; IPR005639; endotoxin_N.
DR InterPro; IPR008979; Gal bind like.
DR Pfam; PF03944; Endotoxin_C_1_
DR Pfam; PF00555; Endotoxin_M; 1_
DR Pfam; PF03945; Endotoxin_N; 1_
RC STRAIN=INA67;

KM Sporulation; Toxin.
FT CONFLICT 338 338 V -> I (in Ref. 2).
FT CONFLICT 382 382 G -> A (in Ref. 2).
FT CONFLICT 1002 1002 V -> I (in Ref. 2).
FT CONFLICT 1012 1012 E -> K (in Ref. 2).
FT CONFLICT 1053 1053 Missing (in Ref. 2).
FT CONFLICT 1085 1085 G -> R (in Ref. 2).
SQ SEQUENCE 1169 AA; 132284 KM; EPCAF6F6E7BC1E CRC64;

Query Match 8.1%; Score 207.5; DB 1; Length 1169;
Best Local Similarity 22.7%; Pred. No. 2.1e-06;
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

QY 10 ITQRIILDNFIKITYAKL-QFTNQSDIQ-----YFVL 41
DB 95 ITTLRGLDSYEVYLEALREWEENPNNAQLREDVRIRPANTDALLITAINFTLTSFEIP 154
QY 42 TLPLRAQCNWMLMLKQATISVWGQQLDSQNLGKYLRLKVYINDVNTYNOGLE 101
DB 155 LLSTVYQANLHLSLRLDAVSFGQGWGIDIAVTNNHNYRLINLHRYEHLDTYNOGLE 214
QY 102 LEKAPLNVSDPEEYLAQRPDISVLRSNFKEWKMNVAKYKRGMAASLSLALPPTF 161
DB 215 -----NLRGINTRO---MSRFNFRRLTLTVLDIYALFPNY 248
QY 162 GPN-VPKQALKVQSRQIF-----APV-IGIPGITSQDSGPTFGSMRPDVKTYYDID 212
DB 249 DARAVPIQTSSQL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVAPPHLMD 298
QY 213 ALRQMLEIYIPLKASATW--IYESDMKVRATYVNDYIGKRGSTNGAAMHMMSSDPSAIY 270
DB 299 FWNLSLF-VTAATVVSQTVWGCHLVSRNTAGNPINFPYGVNPGGALW-TADEDPPEY 356
QY 271 TS-----ALGAGYAPNVGVNR-----YSHGSGYTKGM-----APANTNAYAPF 309
DB 357 RTLSDPVRVRRGFGPNPHVLLRGVGGQQTGTNHTTRFRNSGCTDSIDEIPQNSGAPW 416
QY 310 E-----FRYPGYKLSVSAVYGSKAPDADSVMEFPRVLIENANQLITDTAL 358
DB 417 NDYSHVLNHTVFPVWPG---EIASDSWRAP-----MFSWTH-RSADRTNIINPNIIT 465
QY 359 QIPA-----BIGITDV-VPAFGRTEEPINGODAIRIMESFTSGFG-FTYVDSPOKOKY 410
DB 466 QIPAVKANLHSGSTVVRGPGF-----TGGDLRL-RITVGTFFADIRVNIITGLSQRY 516
QY 411 KIYRIANNLSASTVSLTYNNQTFETDILNTSLDPNGVGNVGSYTLVEGPIL----- 464
DB 517 RVRIRY-----ASTTDL-----QFTTRINGTSVN-----QGNF--QRTMNRGDNLESNGNFR 561
QY 465 -----FSGGTNIFKLGSQ---KGEFADSIIFSP 490
DB 562 AGFSTPFSFNAOSTFTLTGTQAFSNOEYVIDRIEFVP 598

RESULT 13

Q45749

ID_Q45749 PRELIMINARY; PRT; 1174 AA.

AC Q45749;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Crystal protein (Crystal delta-endotoxin).
GN Name=cryIpb;
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

CC NCB1_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RA Lambert B.;
RL Submitted (Apr-1993) to the EMBL/GenBank/DBJ databases.

CC [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B-Pf-86;

RA Li C., Zhang J., Huang D., Li G.
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; Z22512; CA80235.1; -
 DR EMBL; AF336114; AA013295.1; -
 DR PIR; S32649; S32649.
 DR HSSP; P02965; 1CIY.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal bind_like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 SQ SEQUENCE 1174 AA; 133350 MW; 8C7F122F9446F15C CRC64;

Query Match 8.1%; Score 207.5; DB 2; Length 1174;
 Best Local Similarity 22.7%; Pred. No. 2.2e-06;
 Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

QY 10 ITQRIINDNFIKYIAKL-QPSTNGSDIQ-----YDVL 41
 DB 95 ITTRKGLADSYEVYLEALREWEENNNNAQLREDVIRFANTDDALITANNFTLTSFEIP 154
 QY 42 TLPLRAQCVWHMLLKATTSVWQQIDSQLNGYKALIRLIRKYTNVDVNTYNOGLE 101
 DB 155 LLSVYQAANHLHLRLDAVSPGQMGDLITVNNHYNRLINLHRYEHCLDITYNOGLE 214
 QY 102 LEKAPFLNYSDBEYVLQGRPDISVLRNFKKVMKNNVAKYKRGMASSALSLALPTFE 161
 DB 215 -----NLKGTNTRQ--WSFPNQRRLTLITVDIYALFPNY 248
 QY 162 GPN-YPKQALKVVSROIF-----APV-IGIPGIGTSODSGPFGSMRFPDKTYDID 212
 DB 249 DARAVPIOTSSQL-TREITYTSVIEDSPVSNIPMG-----FNDAEFGVRPHLMD 298
 QY 213 ALRQIMELIYQPLKSAFYW--IYESDMKYRATYVNDYIGKRGSTGALHMMSSPSPALY 270
 DB 299 FNNSLF-VTAETVRSGTQWGHLYSSRNTAGNPINFPIYGIENPGALW-LADEBPRDFY 356
 QY 271 TS-----ALGAAGVAPNVGV-----YSHGGSYTKGM-----APANTVAVAP 309
 DB 357 RTLSDPVRVGRGFGPHYVLGLRGVAFQGTGNNHRTTRNSGTISLSDEIPQDNGAPW 416
 QY 310 E-----FKYPGYKLHSVSAVGLSKAPDAADSVMFGRPVLLNEANQLITDTAL 358
 DB 417 NDYSHVLNHYTFVRMPG---EIASDSWRAP-----MFSWTH-RSADRTNIIINPNIIT 465
 QY 359 QIPA-----EIGITDV-VPAFGTEEPINGODAIRIESFTSGFG-FTTYVDSPOKQY 410
 DB 466 QIPAVKANHLSGSTVVRGPGF-----TGDDLIR-RITNGTADIRVNTIGLPSORY 516
 QY 411 KIIVIANNLASVSLTYNNOTFEFTDLINTSLDNGVRGNVGSATLVGPIIE----- 464
 DB 517 RVRIRY-----ASTTDL-----QFTIRNGTSVN---QGNF-QRTNMRGNLBSGNPRT 561
 QY 465 -----FSQGTNIFKLGSQ---KGEFADISIIISP 490
 DB 562 AGFSTPFPSPNAGSTFTLGTQAFSNQGVYIDRIEFVP 598

RESULT 14
 Q8RQ06 PRELIMINARY; PRT; 660 AA.
 AC Q8RQ06;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Mosquitocidal toxin (Fragment).
 GN Name=cry39a;
 OS *Bacillus thuringiensis* (subsp. aizawai).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1433;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ito T., Sahara K., Bando H., Asano S.;
 RT "Cloning and Expression of Novel Crystal Protein Genes cry39a and
 RT 39orf2 from *Bacillus thuringiensis* subsp. aizawai Buntl-14 Encoding
 RT Mosquitocidal Proteins."
 RL J. Insect Biotechnol. Sericology 71:123-128 (2002).
 DR EMBL; AB074413; BAB72016.2; -
 DR HSSP; P07130; 1DLC.
 DR GO; GO:0005102; F:receptor binding; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001178; Endotoxin.
 DR InterPro; IPR005638; endotoxin_C.
 DR InterPro; IPR005639; endotoxin_N.
 DR InterPro; IPR008979; Gal bind_like.
 DR Pfam; PF03944; Endotoxin_C; 1.
 DR Pfam; PF00555; Endotoxin_M; 1.
 DR Pfam; PF03945; Endotoxin_N; 1.
 FT NON_TER 1
 SQ SEQUENCE 660 AA; 75643 MW; A32EF6257CB9404 CRC64;

Query Match 8.1%; Score 207; DB 2; Length 660;
 Best Local Similarity 22.8%; Pred. No. 1.1e-06;
 Matches 109; Conservative 62; Mismatches 133; Indels 154; Gaps 23;

QY 13 FRINDNFIKYIAKLQFSTNGSDIQYVLTPLPLRAQCVWHMLLKATTT--SVWQQID 70
 DB 170 FEDVHTFVKDMASIFSATN-----YEVLLPYVAQAANHLHLRLRGVLYGSRWG--I 221
 QY 71 SQLNGYKALIRLIRKYTNVDVNTYNOGLELEKAPFLNYSDBEYVLQGRPDISVLRN 130
 DB 222 AAPADFFHDQLKXTATAYAHCVTYNNGLAQOK-----EL 257
 QY 131 FKEVMKNNKVKYKRGMASSALSLALFPFGPNVYPKQALKVVSROIFAPVIGIPGIT 190
 DB 258 FAKSPNNKRFVAYRDMTITTYLDIALFFTYDALALYKPIITELTREIYSVNLV----- 312
 QY 191 SQDSGPTFGSMRFPDKTYDQ-----IDALRQIMELIYQPLKSAFYWIIYESDMKYRAT 242
 DB 313 -----DVYGVQQTDLINKKEAFAFTRSPHLVTRRG-FPEYTR-TKYAY-----WRYLAG 358
 QY 243 YVNDYIGKRGSTGAAHMMSSDPSATYTSALGAAGVAPNVGVGRYSGSYTKGMAPAN 302
 DB 359 HTN-YFSFTGNGT-----IYSS-----SFNNMYDTDMTKST 388
 QY 303 TNA--VAPFEKPYKYLHSVSAVGLSKAPDAADSVMFGRPVLLNEANQLITDTALQI 360
 DB 389 INIDPYANI-----YKIMTSTYNISPYTDPV-----GISOMQPSLTNNQOLTYTGTSA 437
 QY 361 PA-----EIGITDVVPAFGTEEPINGODAIRIESFTSG--FGFTTYVDSPOKQY 410
 DB 438 PKYVARETFEIPPTD-----EKPLTYENYSHILSYMSAHHFG-----DK 478
 QY 411 KIIVIANNLASVSLTYNNOTFEFTDLINTSLDPN-----GVRNGVSTTLV-EGP 461
 DB 479 KIGYTFA-----WMHESYDFDNR-----VDPDKITQIPAVKGYLQGVYKQGP 522

RESULT 15
 C1FA_BACTA STANDARD; PRT; 1174 AA.
 ID C1FA_BACTA
 AC Q03746;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Pesticidal crystal protein cryIa (Insecticidal delta-endotoxin
 DE CryI(a)) (Crystalline entomocidal protoxin) (134 kDa crystal protein).
 GN Name=cryIa; Synonyms=cryIa, cryI(a);
 OS *Bacillus thuringiensis* (subsp. aizawai).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OK NCBI_TaxID=1433;
 RN [1]
 RC STRAIN=EG6346;
 RX MEDLINE=91286178; PubMed=2061280;
 RA Chambers J.A., Jelen A., Gilbert M.P., Jany C.S., Johnson T.B.,
 RT Gawron-Burke C.,
 RT "Isolation and characterization of a novel insecticidal crystal
 RT protein gene from *Bacillus thuringiensis* subsp. *altawai*."
 RL J. Bacteriol. 173:3966-3976(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NRRL B-18484 / P6811;
 RA Payne J.M., Sick A.J.;
 RT "Bacillus thuringiensis isolate active against lepidopteran pests, and
 RT genes encoding novel lepidopteran-active toxins."
 RL Patent number US5188960, 23-FEB-1993.
 CC -!- FUNCTION: Promotes colloidsmotic lysis by binding to the midgut
 CC epithelial cells of many lepidopteran larvae.
 CC DEVELOPMENTAL STAGE: The crystal protein is produced during
 CC sporulation and is accumulated both as an inclusion and as part of
 CC the spore coat.
 CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-
 CC terminus.
 CC -!- SIMILARITY: Belongs to the delta endotoxin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL/ M63897; AAA22348.1; -
 DR EMBL/ M73254; AAA22347.1; -
 DR PIR/ A42459; A42459.
 DR HSSP/ P02965; 1C1Y.
 DR InterPro/ IPR001178; Endotoxin.
 DR InterPro/ IPR005638; endotoxin_C.
 DR InterPro/ IPR005639; endotoxin_N.
 DR InterPro/ IPR008979; Gal bind like.
 DR Pfam/ PF03944; Endotoxin_C_1.
 DR Pfam/ PF00555; Endotoxin_M_1.
 DR Pfam/ PF03945; Endotoxin_N_1.
 DR Sporulation; Toxin.
 SQ SEQUENCE 1174 AA; 133621 MW; B51B9751D7F91C61 CRC64;
 Query Match 7.8%; Score 200; DB 1; Length 1174;
 Best Local Similarity 22.0%; Pred. No. 7.8e-06;
 Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;
 QY 10 ITQPRILNDNFIKYIAKL-QFSTNOSDLO-----YPLV 41
 DB 95 ITTLGLADSYEITYEALREWEANPNNAQLREVRIRFANTDDALITAINNFTLSFEIP 154
 QY 42 TPLRAQACVHMLMLIKDATTSVWGQOIDSQOLNGYKALIRLIKVTNDVNTYNOGLE 101
 DB 155 ILSVYVQAANLHLSLRLDAVSFGQGWGLDIATVNNHYNRLINLHRYTGHGCLDTYNOGLE 214
 QY 102 LEKAPKINSDEBEYIQAQRPDISVLRSPKVEVMKNKAKYKRGMAAGSLAALFPTF 161
 DB 215 -----NLKGTNTRQ---WARFNPQRRLDTLTFLDIALFPMY 248
 QY 162 G-PNYPKQALKVVSQRIE-----APY-IGIPGIGTSQDSGPTFGSMRFDVKYTDQID 212
 DB 249 DVRTYPIQITSSQL-TREITSSVIEDSPYSANIPNG-----FNRAEFGVRRPHLMD 298
 QY 213 ALRQIMELYIQPKSAYFYIYSSDWKVRATYVNDYIGKRG-----NTGAAMHMMSSD 265
 DB 299 FNNSLF-VTAETVRS-----QTVMGHILVSSRNTAGNINIPPSYGVFNPAGAIWIADBD 351
 QY 266 PSAIYTS-----ALGAGYAPNVVGVV-----YSHGGSYTKGM-----APANTN 304

DB 352 PRPFYRTLSDPVVRKGGFGNPHYVLGLRGVAFOQTGNTHTFRNSGTIISLDEIIPODN 411
 QY 305 AYAPPE-----FKYPGYKLHSVASAYGLSKAPPAADSVWGFPPVLLNEANQL 353
 DB 412 SGAPWMDYSHLVNHTFVRWPG-----EISGSDSWRAP-----WFSWTH-RSAPFTNTID 460
 QY 354 TDTALQIP-----AEIGITDV-VPAFGRTPEIPINGODAIRIWESFTSGFGFTYTV--- 402
 DB 461 PERITQIDPLVRAHTLQSGTIVVRGPGF-----TGCDILR-----RTSGGPFAYTIIVNIN 509
 QY 403 -DSPQKQKKIIRANNLASATVSLTYNNQTFPTDINTSLDPNGVAGNGSY----- 455
 DB 510 GQLPQRYRARIKYASTNL---RIVTVAGSRIFAGQFNKTMW-TGDPFTQSFYSYATIN 565
 QY 456 TLVEGPITE--FSQGTNIFKLQSGKGEPAIDSIIFSPV 491
 DB 566 TAFTPMGSSTFTVADTFSSGN---EYIDRFELIP 600

Search completed: October 19, 2005, 20:17:43
 Job time : 182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:08:58 ; Search time 44 Seconds

(without alignment)
834.712 Million cell updates/sec

Title: US-10-756-778-8

Perfect score: 2560

Sequence: 1 IAEPPSTGVITQFRLINDNF.....KLGSQKGFALDSITFSPV 492

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	225.5	8.8	1138 1	US-07-973-320-2
2	225.5	8.8	1138 1	US-07-973-320-4
3	223.5	8.7	1169 1	US-08-542-921-2
4	223.5	8.7	1169 2	US-08-880-685-2
5	223.5	8.7	1169 2	US-08-880-684-2
6	210.5	8.2	1167 1	US-08-100-709-2
7	210.5	8.2	1167 1	US-08-176-865-2
8	210.5	8.2	1167 1	US-08-474-038-2
9	210.5	8.2	1167 2	US-08-779-046-2
10	210.5	8.2	1167 2	US-08-881-340-2
11	207.5	8.1	1168 1	US-08-291-368-4
12	207.5	8.1	1168 2	US-08-962-190-4
13	207.5	8.1	1168 5	PCT-US95-10310-4
14	200	7.8	605 3	US-09-178-252-4
15	200	7.8	605 4	US-09-826-660-4
16	200	7.8	718 2	US-08-731-079A-1
17	200	7.8	1148 1	US-08-349-867-23
18	200	7.8	1148 1	US-08-349-867-27
19	200	7.8	1148 1	US-08-239-476-23
20	200	7.8	1148 2	US-08-239-476-27
21	200	7.8	1148 2	US-08-598-305A-23
22	200	7.8	1148 2	US-08-598-305A-27
23	200	7.8	1148 2	US-08-598-305A-35
24	200	7.8	1148 2	US-08-598-305A-37
25	200	7.8	1148 2	US-08-598-305A-38
26	200	7.8	1148 2	US-08-639-923A-23
27	200	7.8	1148 2	US-08-639-923A-27

28	200	7.8	1148 2	US-08-639-923A-35	Sequence 35, Appl
29	200	7.8	1148 2	US-08-639-923A-37	Sequence 37, Appl
30	200	7.8	1148 2	US-08-639-923A-38	Sequence 38, Appl
31	200	7.8	1148 3	US-09-178-252-2	Sequence 2, Appl
32	200	7.8	1148 4	US-09-826-660-2	Sequence 2, Appl
33	200	7.8	1148 5	PCT-US95-05431-23	Sequence 27, Appl
34	200	7.8	1148 5	PCT-US95-05431-27	Sequence 10, Appl
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36	200	7.8	1174 1	US-08-349-867-25	Sequence 29, Appl
37	200	7.8	1174 1	US-08-349-867-29	Sequence 32, Appl
38	200	7.8	1174 1	US-08-349-867-32	Sequence 29, Appl
39	200	7.8	1174 1	US-08-239-476-25	Sequence 29, Appl
40	200	7.8	1174 1	US-08-239-476-29	Sequence 8, Appl
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43	200	7.8	1174 2	US-08-598-305A-29	Sequence 32, Appl
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45	200	7.8	1174 2	US-08-639-923A-32	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-07-973-320-2
Sequence 2, Application US/07973320
Patent No. 5286486
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/973,320
FILING DATE: 19921106
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/788,638
FILING DATE: 6-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA68.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1138 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus thuringiensis
STRAIN: dakota
INDIVIDUAL ISOLATE: HD511
IMMEDIATE SOURCE:

```

1      LIBRARY: Lamsdgem (TW)-11 Library of J.M. Fu
2      CLONE: 511
3      US-07-973-320-2
4
5      Query Match      8.8%; Score 225.5; DB 1; length 1138;
6      Best Local Similarity 22.5%; Pred. No.1.1e-12;
7      Matches 126; Conservative 75; Mismatches 207; Indels 151; Gaps 25
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9      QY      7      TGVITOPILNDNFYKIAKLOFSTNSQDLOYPVLTLPRAQCVNHLMLKDATF--SV 64
10     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
11     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
12     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
13     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
14     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
15     DB      155     TRVIDRFRILDALFESYMPSEFVA-----GYEIPLTIVYAQAMHLALLRDSITLYGBK 208
16
17     QY      65      WG--QIDISQOLNGKAEILIRIKYTYNDVNTTNOGLELEKAKPLNTSDPEEYIQAGRP 122
18     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
19     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
20     DB      209     WGFPTNNIIEENNRK--KHISEYSHVCVMYNSGS----- 243
21
22     QY      123     DISVLSNPFKEVMKNNKVAKYRGNAMSALSTAALFPFPGPNVYKQALKYVQSRQIFAV 182
23     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
24     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
25     DB      244     -----RANGSYTEQMINNRRPREKILMWLDIAAVFPYIDPRMYSMETSTQLTREYTPD 298
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27     QY      183     IGIPGIGITSODSGPTFGSMRPDV-KTYDQIDALRLMLIYIOPK-----SAYFW 231
28     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
29     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
30     DB      299     ISL--SISNPDIGPFSQMENTAFRTPLHLV--YLDELIXITYSKYKAFSHEIOPDLFYW 353
31
32     QY      232     -IYESDMKVRATYVNDYIGKGSNTGAMHMMSSDPSAITYTAL--GAAGYAPNVYGVY 288
33     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
34     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
35     DB      354     CVHAKSFK-----KSEOSMLYTTGIIGKTSY--ISSGAY 386
36
37     QY      289     SHGS--YTKGMAPA-----NTNAYAPFEEKYRGYKLIH--SVSAYGSKAPDAADSVY 337
38
39     DB      387     SFRGNDIYRTLAAPSVVYPTQNTGVGEVEYGVKGVHNYRGDKYDILTY--DSIDQLP 444
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41     QY      338     FGFRPVLLLENANQLLTDTALQIPAEIGITDVVPAGRTE-----EPINGODAI 386
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46     QY      387     RIWE-----STSGRGFT-----YTVDSPOKOKYKIIYIANNLSA-- 422
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49     DB      504     KMYKLDLSTVVKGPGFTGDLVKRGSNGYIGDIKATVNSPQSKYRVRVYATSVSGLF 563
50
51     QY      423     -----STVSLVYNNOTFFTDILNTSLDPNGVAGNGYSYTLVE-GPIEESQGTNIFKJ- 475
52     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
53     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
54     DB      564     NVFINDELTALQKNPOSTVETI-----GEGKDLTYSFYEIYESTTTOPEPNHPKITLHL 617
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56     QY      476     --SOKGEFAIDSIIFSPV 491
57     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
58     |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
59     DB      618     NHLSNNSPFYVDSIEFIV 636
60
61     RESULT 2
62     US-07-973-320-4
63     ; Sequence 4, Application US/07973320
64     ; Patent No. 5286486
65     ; GENERAL INFORMATION:
66     ; APPLICANT: Payne, Jewel M.
67     ; APPLICANT: Fu, Jenny M.
68     ; TITLE OF INVENTION: No. 5286486el Bacillus thuringiensis Gene
69     ; TITLE OF INVENTION: Encoding a Coleopteran-Active Toxin
70     ; NUMBER OF SEQUENCES: 4
71     ; CORRESPONDENCE ADDRESS:
72     ; ADDRESSEE: David R. Saliwanhik
73     ; STREET: 2421 N.W. 41st Street, Suite A-1
74     ; CITY: Gainesville
75     ; STATE: FL
76     ; COUNTRY: USA
77     ; ZIP: 32606
78     ; COMPUTER READABLE FORM:
79     ; MEDIUM TYPE: Floppy disk
80     ; COMPUTER: IBM PC compatible
81     ; OPERATING SYSTEM: PC-DOS/MS-DOS
82     ; SOFTWARE: Patentin Release #1.0, Version #1.25
83     ; CURRENT APPLICATION DATA:
84     ; APPLICATION NUMBER: US/07/973.320

```

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1 FILING DATE: 19921106
2 CLASSIFICATION: 435
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 07/789,638
5 FILING DATE: 6-NOV-1991
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Saliwanchik, David R.
8 REGISTRATION NUMBER: 31,794
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: 904-375-8100
11 TELEFAX: 904-372-5800
12 INFORMATION FOR SEQ ID NO: 4:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 1138 amino acids
15 TYPE: AMINO ACID
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: protein
19 HYPOTHEICAL: YES
20 ANTI-SENSE: NO
21 ORIGINAL SOURCE:
22 ORGANISM: Bacillus thuringiensis
23 STRAIN: kumamotoensis
24 INDIVIDUAL ISOLATE: HD867
25 IMMEDIATE SOURCE:
26 LIBRARY: Lamdagem (TM) -11 library of J.M. Fu
27 CLONE: 867
28 US-07-973-320-4
29
30 Query Match 8.8%, Score 225.5; DB 1; Length 1138;
31 Best Local Similarity 22.5%; Pred. No. 1,1e-12;
32 Matches 126; Conservative 75; Mismatches 207; Indels 151; Gaps 25
33
34
35 7 TGVITQPIILNDNFIKYIAKLQFSGNSDLDQPVLTLPBPAQACWHLMLKDATT--SV 64
36 155 TRVIDRFLIDALFESTYSPFRVA----GELPLTLVYQANLIALALDSTLYGDK 208
37 65 WG--QQIDSQQLANGYKALLRLIKVYTDVNTVYNOGLEKAKPLNYSDEEYLAQGRP 122
38 209 WGFQNNIEEYVNNQK---KHISEYSHCVKWNISGLS----- 243
39 123 DISVLRNFEKVMKKNKAKYKRGKMANSSALSALPPTFGPNYPKQALKVVOSSROI 182
40 244 ----RLNGSTYEOMINYNRRFRREMILMVLDIAAVFPYIDPRMYSMETSTQLRE 298
41 183 IGIQGGITSDSGPTFGSMRFDV-KTYQIDALQMLXYIQPLK-----SAYFW 231
42 299 ISL--SISNPIGSPFSOMENTARFTPLVD--YLDELVYITSYKKAFSHEIOPDLFW 353
43 232 -IYESDWKVRATVYNDYIGKRGSNVGAAMHMMSSDPSAITYSAL--GAAGYAPNVGV 288
44 354 CVHKVSKF-----KSEQSNLYTTGIGKTSGY---ISSGAY 386
45 289 SHGGS--YTKGMABA-----NTNAYAPPEFYKPGYKLN---SVSAYGLSKAPDA 337
46 387 SFRGNDIYRTLAASVVVYPTQYVGVQVEFYGVKGVHVRGDKYKLDLY--DSID 444
47 338 FGFRPVLLENANQLIDTALQIAEIGITDVVPAGFTE-----EPINGDAI 386
48 445 PDGEPRI-HEKTHHLCAVTAISKSTPDYDNATIPRFSWTHRSABEYNNRIYPNK 503
49 387 RIWE-----SPTSGFGFT-----YVDPSPQOKOKYKLIYRIANNLSA-- 422
50 504 KMYKLDLSTLVKKGPGFTGDLVVRGSGNGYIGDIKATVNSPLSQKTRVRKRVANS 563
51 423 -----STVSLYNNQTFETDILNTSLDPNGVRGVNGYSATLVE-GPIIEFSO 475
52 564 NVFINDELALQKNQSYVETI-----GEGKDLTYGSGYIEYSTTIGFRNHRK 617
53 476 ---SOKGEFAIDSIIFSPV 491
54 618 NHTLSNNSPFYVDSIEFIPV 636
55 DB

```

RESULT 3
US-08-542-921-2
; Sequence 2, Application US/08542921
; Patent No. 5736514
; GENERAL INFORMATION:
; APPLICANT: IIZUKA, TOSHIHIKO
; APPLICANT: TAGAMA, MICHITO
; APPLICANT: ARAI, SATOSHI
; APPLICANT: NITZEKI, MASATSUGU
; APPLICANT: MIYAKE, TOSHIRO
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/542,921
; FILING DATE: 13-OCT-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 276082/94
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 49-209-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-542-921-2

Query Match 8.7%; Score 223.5; DB 1; Length 1169;
Best Local Similarity 22.3%; Pred. No. 1.8e-12;
Matches 130; Conservative 78; Mismatches 192; Indels 183; Gaps 30;

QY 9 VITQRIANDNPRIKIALQSTNSDQYPLVTLPLRAQAVMMLIKATT--SWWG 66
DB 168 VSQRNILDLSLEPTQMP--SFSGSGSQNYATILPLVAAANLLELLKCDIYGARWG 225
QY 67 QOIDSQQLNGYKAEILRIKVTYNDVNTYNOGLELEKAKPLANYSDPEEYLQAGRPIISV 126
DB 226 --LWQTQIDQPHSRQOSLTQYITNHCVTAYNDL-----AE 259
QY 127 LRSNFEVWKNNKVAKYRGAMASLSAALPFTGPNYPKQALKVQSRQIFAVIGI- 185
DB 260 LRGTAAE--SWFKYQYRREMTLTAMDIALPYPYNLRQYDPDGTNPDLREYVTDPIAFD 317
QY 166 -----PGGITSQ-----DSGPTF-GSMRPVY-----KITDQIDALRQMLELYIOPLK 226
DB 318 PLEQP--TTQCRSMYINPARNHLNFSVLENSLIRPHELRLSNQILVN--YQING 372
QY 227 SA-----YFWIYESDMKVRRA--TYVNDYIGKR-----GSNTGAAMH 260
DB 373 SAMRGSRRVRYHLSHSIIQKSKSYGLSLDPVGANINVQNNDIYQIISQVSNFASPVGSSYS 432

QY 261 MWSSDPSAIYTSA---LGAAGYAPNVVGV-----RYSHGGSY 294
DB 433 VMDTN---FLLSSQGVGISGYTQGGIPAVCLQQRNSTDLEPISNPEGDIIRNYSRHLSH 489
QY 295 -----TGKMAPANTNAYAPPEFKYPGYKLSVSAVGLSKADADSWVFGFRPVLE 346
DB 490 ITQYRFQATQSGSPSTVSANLP-----TCWTHRDVLDL 523
QY 347 N--EANOGLDUTLALQIP-----AEIGITDVV--PAFGRTEEPINGODAIRMESFTSGFG 397
DB 524 NTTANQI-----TQLPVKAYELSSGATVYKGBF-----TGSDVIR--RNTGFGF 569
QY 398 -FYTVDSPQOKYKIYRIANMLSAS---TVSLTYNNQTFETDILNTSLDPNGRGANYG 453
DB 570 AIRSVATGPLQRIIRIFRYASTIDFDFVTRGGTTINFRFTRWK-----RQESRYE 624
QY 454 SYTLVEGPI-IEESQGNIFPLGSQ---KGEPAIDSIITSPV 491
DB 625 SYRTVEFTPEFNFQOSODIIRTSIQGLSGNGEVYLDRIEILIPV 667

RESULT 4
US-08-880-685-2
; Sequence 2, Application US/08880685
; Patent No. 5834296
; GENERAL INFORMATION:
; APPLICANT: IIZUKA, TOSHIHIKO
; APPLICANT: TAGAMA, MICHITO
; APPLICANT: ARAI, SATOSHI
; APPLICANT: NITZEKI, MASATSUGU
; APPLICANT: MIYAKE, TOSHIRO
; TITLE OF INVENTION: NOVEL BACILLUS STRAIN AND HARMFUL
; TITLE OF INVENTION: ORGANISM CONTROLLING AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,685
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/542,921
; FILING DATE: 13-OCT-1995
; APPLICATION NUMBER: JP 276082/94
; FILING DATE: 14-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 49-209-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-880-685-2

Query Match 8.7%; Score 223.5; DB 2; Length 1169;


```

APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESS: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/100,709
FILING DATE: 1993/07/29
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-100-709-2

Query Match
Beet Local Similarity 21.9%; Score 210.5; DB 1; Length 1167;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

3 EPPSTGVITOPRIINDNFIAKIQFSTNOSDLOYPVLTPLRAQACWMLMLKDATY 62
123 EAAKSRVDRFRILDLGLEANIIPSPRI-----IGFEVPLLSVYQANLHLALRDSV- 175
63 SWGQO--IDSOQLNGYAEILRLIKVTNDVNTTNOGLEKAKPLNTSDPEYLOAG 120
176 -IFGRMWGLTKVNDIYNROIIEHYSNHCVDYNTLE----- 215
121 RPDISVLSNFKKWKMKVAKYKRGMSALSIALPPTGPN-YPKQALKVQSRQIF 179
216 -----RLGFRSLAQMRIVNQFRRELITVLDIVALFPNYSRLYPIQTSQLTREIVT 268
180 APVIGIPGIGITSDSGPTFGSMRFDVKTYDQIDALROL-----MELYIQLKSAFW-- 231
269 SPVSEFYGVLT--NSGNIIGTL-----TEQOIRRHPLMDPFSNMTIMYSDNRREHYWSGL 321
232 ---IV-----ESDWKVRATVND-----YIGKR 251
322 EMTAFTGPAQOVFPFLVGTGREGSAPPLTVRSVNDGIYRILSAPFYSAPFLGTTVLGSR 381
252 GSNLTGAAMMMSSDPAIYTSALGAAGYAPNVGVYRSHGSGSYTGKMAPNANTNAYAPFEP 311
382 GKPFDPALNNISPPSTTYRH---PGTVDSLVS1-----PPDONSVP--- 421
312 KPGYKLSHVSAYGLSKAPDAADSVWFGF--RPVLLENANQLTDTALQIPAEIGITDV 369
422 -----HFGSHRLSHVTMRASSPIFHHTHSATTNTIN--PVALIQIP-----L 464
370 VAPGHTPEPINGQDAIRIWESFTSGFGFT-----YVDSPOQOKXI 412
465 VAFANLH---SGATVVR-----GPGTGDDILARTNTGTFADMRVAVITGPLSQRYAV 513
413 IYRIANNLSASTVSLTYNNQTFETDILNLSLPNGVRGNVGSYTLVEGPIIE----- 464

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DB 514 RIRY-----ASTDPL-----OFFTRINGTSVN-----OGNF-QRTMRGNDLNSGNFRTAG 558
CY 465 -----FSQGNIFKLGSO---KGEPAIDSLIFSP 490
DB 559 FSTPSPSNASTFTLTGTOAFPSNOEYIDRIEFPV 593

RESULT 7
US-08-176-865-2
Sequence 2, Application US/08176865
Patent No. 5616319
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yiping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.
TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Panitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESS: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,865
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-865-2

Query Match
Beet Local Similarity 21.9%; Score 210.5; DB 1; Length 1167;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

3 EPPSTGVITOPRIINDNFIAKIQFSTNOSDLOYPVLTPLRAQACWMLMLKDATY 62
123 EAAKSRVDRFRILDLGLEANIIPSPRI-----IGFEVPLLSVYQANLHLALRDSV- 175
63 SWGQO--IDSOQLNGYAEILRLIKVTNDVNTTNOGLEKAKPLNTSDPEYLOAG 120
176 -IFGRMWGLTKVNDIYNROIIEHYSNHCVDYNTLE----- 215
121 RPDISVLSNFKKWKMKVAKYKRGMSALSIALPPTGPN-YPKQALKVQSRQIF 179
216 -----RLGFRSLAQMRIVNQFRRELITVLDIVALFPNYSRLYPIQTSQLTREIVT 268
180 APVIGIPGIGITSDSGPTFGSMRFDVKTYDQIDALROL-----MELYIQLKSAFW-- 231
269 SPVSEFYGVLT--NSGNIIGTL-----TEQOIRRHPLMDPFSNMTIMYSDNRREHYWSGL 321

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QY      232  ---LY-----ESDMKRAATYYND-----YIGKR 251
Db      322  EMATAYFTGAGAQVSPFLVGTGREGSAPPLVTASVNDGIYRILISAPFYSAPELGTIVGSR 381
QY      252  GSNTGGAAMHMSSDPBAITYTSLAAGAAGYAPNVVGRYRSHGSGSYTKGMAAPANTAYAPFEF 311
Db      382  GEKFPDALNNISPPSTIYR--PGTVDSIVSI-----PPDDNSVVP--- 421
QY      312  KYRGYKLHSVSAAGSKAPDADSVMFGE--RPVLLENEANQLTDPTLQIPAEIGITDV 369
Db      422  -----HGSSHRLSHVTMRBASSPLFHHHTHSATTNTIN---PMLIQIP-----L 464
QY      370  VPAFGTEEPINGQDAIRIWESFTSGFGT-----YTUDSPQCKYKKI 412
Db      465  VKAFNLH-----SGATVVR-----GPGFTGGDILRTNTGTFTADMVRNVIITGSPLSQRYR 513
QY      413  IYAIANNLASATVSLTYNNQTFETDILNLSLDPNGVGRNGSGSYTLVBSPII----- 464
Db      514  RINY-----ASTDDL-----QFFTRINGSVN-----QGNF--QRTMNRDNLESGNPRTAG 558
QY      465  -----FSQCNTIFKLGSQ---KGEPAIDSIIFSP 490
Db      559  FSTPFSFSAQAQSTFLGTQAFSNOEYVYDRIIEFVP 593

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1      RESULT 8
2      US-08-474-038-2
3      / Sequence 2, Application US/08474038
4      / Patent No. 5679343
5      / GENERAL INFORMATION:
6      / APPLICANT: Donovan, William P.
7      / APPLICANT: Tan, Yiping
8      / APPLICANT: Jany, Christine S. M.
9      / APPLICANT: Gonzalez Jr., Jose M.
10     / TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
11     / TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
12     / NUMBER OF SEQUENCES: 5
13     / CORRESPONDENCE ADDRESS:
14     / ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
15     / ADDRESSEE: Nadel
16     / STREET: 1601 Market Street, 36th Floor
17     / CITY: Philadelphia
18     / STATE: Pennsylvania
19     / COUNTRY: U.S.A.
20     / ZIP: 19103
21     / COMPUTER READABLE FORM:
22     / MEDIUM TYPE: Floppy disk
23     / COMPUTER: IBM PC compatible
24     / OPERATING SYSTEM: PC-DOS/MS-DOS
25     / SOFTWARE: Patentin Release #1.0, Version #1.25
26     / CURRENT APPLICATION DATA:
27     / APPLICATION NUMBER: US/08/474,038
28     / FILING DATE: 07-JUN-1995
29     / CLASSIFICATION: 514
30     / PRIOR APPLICATION DATA:
31     / APPLICATION NUMBER: US 08/176,865
32     / FILING DATE: 30-DEC-1993
33     / APPLICATION NUMBER: US 08/100,709
34     / FILING DATE: 29-JUL-1993
35     / ATTORNEY/AGENT INFORMATION:
36     / NAME: Egoif, Christopher
37     / REGISTRATION NUMBER: 27633
38     / TELECOMMUNICATION INFORMATION:
39     / TELEPHONE: 215-757-1590
40     / INFORMATION FOR SEQ ID NO: 2:
41     / SEQUENCE CHARACTERISTICS:
42     / LENGTH: 1167 amino acids
43     / TYPE: amino acid
44     / TOPOLOGY: linear
45     / MOLECULE TYPE: protein
46     / US-08-474-038-2

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Query Match	8.2%;	Score 210.5;	DB 1;	Length 1167;
Best local Similarity	2.9%;	Pred. 21.5;	4e-11;	
Matches 126;	Conservative 70;	Mismatches 188;	Indels 191;	Gaps 26;
QY	3	EPSPSTGVITQPRILNDNFPIKYLAKQFSTNSDLOQYPVLTLPURQACVHMLMLKDATT	62	
DB	123	EAKSKSVIDRFRIIDILDEIANIPSPRI-----IGFEVPLTSVYQAAHLHALLRDSY-	175	
QY	63	SWAGQO--IDSQOLNGYKAEILRLIKVYNVDVNTYTNQGLEBKAKPLNYSDBEETLQAG	120	
DB	176	-IGERWGLTTKKVNDIYNRQRIREIHEYNHCDVINTLE-----	215	
QY	121	RPDISVLRSNFKEVMKKNVAKYKRYKAMASALSALAPFTFGN-YPKQALKVYOSRQIF	179	
DB	216	-----RLGFRRIAQRIRYNGRERRELTITVDIALFPNYSRLPIQTFSQLREIYT	268	
QY	180	APVITGIGGITSODSGPTGSMRFVQYKTDQIDALRQL-----MELYIPLKSAFW---	231	
DB	269	SPVSEFYGYVI--NSGNIIGTL-----TEQOIRRPRLHLPFNSMIMYTSDNREHYGSL	321	
QY	232	---LY-----ESDMKRAYTVND-----YIGKR	251	
DB	322	EMTAIYTTGFRAGAOVSPPLVGTGRGESAPLTVBSVNDGIIRIISAPYSAPFGLTYLGR	381	
QY	252	GSNTGAMMHMSSDPSAIYTSALGAGVAPNVYGVARYSHSGSYTKGMADPANTNAYAFEEF	311	
DB	382	GEKFDPLANNISPPSTIYRH-----PGTVDSLVS I-----PQONSVP---	421	
QY	312	KYGYKLIHSVANGSLKAPDADSVWFG--RPVLLENANQLDITLQIPAEIGITDV	369	
DB	422	-----HROSSHRLSHVTRASSPFFHTHRSATTTNTIN--PNAIIQIP-----L	464	
QY	370	VPAFGRTEBPINQODAIRIWESFTSGFGTL-----YTVDSPOKQYKI	412	
DB	465	VKAFNLH-----GSATYVR-----GPGTGGDILKRTYTGFPADKRVNIITGPBLSGRYV	513	
QY	413	IYRIANNLSASTVSLTYNNQTFEFTDILNTSLDPNGVNGVYGSYTLVEGP IIE-----	464	
DB	514	RIRY-----ASTLDL-----QFETTRINGTSVN-----QGNF--QRTMGRGNLTSGNFRTAG	558	
QY	465	-----FSQGTNIFKIGSQ--KGEFAIDSIISFP	490	
DB	559	FSTPFSFNAQSTFTLTGQAFSNOEYVDIRIEVP	593	

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1      RESULT 9
2      US-08-779-046-2
3      ; Sequence 2, Application US/08779046
4      ; Patent No. 5854053
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Donovan, William P.
7      ; APPLICANT: Tan, Yuping
8      ; APPLICANT: Jany, Christine S.
9      ; APPLICANT: Gonzalez Jr., Jose M.
10     ; TITLE OF INVENTION: BACILLUS THURINGIENSIS CYET4 AND CYET5
11     ; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
12     ; NUMBER OF SEQUENCES: 5
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Panitch Schartz Jacobs & Nadel c/o A.S.
15     ; ADDRESSEE: Nadel
16     ; STREET: 1601 Market Street, 36th Floor
17     ; CITY: Philadelphia
18     ; STATE: Pennsylvania
19     ; COUNTRY: U.S.A.
20     ; ZIP: 19103
21     ; COMPUTER READABLE FORM:
22     ; MEDIUM TYPE: Floppy disk
23     ; COMPUTER: IBM PC compatible
24     ; OPERATING SYSTEM: PC-DOS/MS-DOS
25     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
26     ; CURRENT APPLICATION DATA:
27     ; APPLICATION NUMBER: US/08/779,046

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FILING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-779-046-2

Query Match 8.2%; Score 210.5; DB 2; Length 1167;
Best Local Similarity 21.9%; Pred. No. 3.4e-11;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

QY 3 EPPSTGVITOPRIINDNFIKYIAKLOFSTNOSDLOQVPLTLPLRAQACVMMHMLIKDATT 62
DB 123 EAASRVIVDRRIIDGLLEANIIPSRF-----IGFEVPLLSVYQANMLIALIRDSV- 175
QY 63 SVMGOQ--IDSQOLNGYKAEILIRLIKVTNDVNTTNOGLELEKAKPLNYSDBEYLOAG 120
DB 176 -IFGRMGLTTKNVNDIYNRQIREIHEYSNHCVDYNTLE----- 215
QY 121 RPDISVLSNFKEMKMKVAKYKRGMAKMSLALFPTGPN-YPKQALKVQVROIF 179
DB 216 -----RLGFRSLAQMRYNQFRRELTLTVLDIVLPNDLSRLYPIQTSQLTREIYV 268
QY 180 APVIGIPGIGITSODSGPTFGSMRFDVKTYDQIDALROL-----MELYIQPLKSAVFW--- 231
DB 269 SPVSEFYGVV--NSGNIIIGTL-----TEQDIRPHLMDFNISMIMTYSNDRREHYWGL 321
QY 232 --IY-----ESDMKVRATVYND-----YIGKR 251
DB 322 EMTAVYFTGFAGAQVSFLVGTGRGESAPPLTVRSVNDGIYRILSAFYSAPFLGTVLGSR 381
QY 252 GSNNGAAMHMMSSDPSAIYTSALGAAGYAPNVGVRSYHSGSYTGMAAPANTNVAPEEF 311
DB 382 GEKFDPALNNISPPSTIYRH---PGTVDSLVS-----PPODNSVPP--- 421
QY 312 KYPGVKLHSVAYGLSKAPDAADSVMEGF--RPVLLENANQLTDTALQIPAEIGITDV 369
DB 422 -----HRGSHRLSHVTMRASSPIFHWTHRSATTNTIN--PMIIQIP-----L 464
QY 370 VPAFGRTPEEPINGODAIRIMESFTSGGFT-----YTVDSPQOKYKI 412
DB 465 VKAFNLH-----SGATVVR-----GPGFTGDIILRRNTGTGFADMRVNIITGPLEQRV 513
QY 413 IYRIANNISASVSLTNNQTFPTDILNTSLDPNGVRKNGSYTVVEGPII----- 464
DB 514 RIRY-----ASTTDL-----QFTTRINGSVN-----QGNF-ORTNKGDNLESNFRTAG 558
QY 465 -----FSOGTNIIFKLGSQ--KGFPAIDSIIFSP 490
DB 559 FSTPFSFSAQSTFTLGTQAFSNOEYVIDRIEFVP 593

RESULT 10
US-08-881-340-2
Sequence 2, Application us/08881340
Patent No. 5942658
GENERAL INFORMATION:
APPLICANT: Donovan, William P.
APPLICANT: Tan, Yeping
APPLICANT: Jany, Christine S.
APPLICANT: Gonzalez Jr., Jose M.

TITLE OF INVENTION: BACILLUS THURINGIENSIS CRYET4 AND CRYET5
TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panlitch Schwarze Jacobs & Nadel c/o A.S.
ADDRESS: Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.

ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,340
FILING DATE: 24-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,709
FILING DATE: 29-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egoif, Christopher
REGISTRATION NUMBER: 27633
REFERENCE/DOCKET NUMBER: 7205-49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-881-340-2

Query Match 8.2%; Score 210.5; DB 2; Length 1167;
Best Local Similarity 21.9%; Pred. No. 3.4e-11;
Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

QY 3 EPPSTGVITOPRIINDNFIKYIAKLOFSTNOSDLOQVPLTLPLRAQACVMMHMLIKDATT 62
DB 123 EAASRVIVDRRIIDGLLEANIIPSRF-----IGFEVPLLSVYQANMLIALIRDSV- 175
QY 63 SVMGOQ--IDSQOLNGYKAEILIRLIKVTNDVNTTNOGLELEKAKPLNYSDBEYLOAG 120
DB 176 -IFGRMGLTTKNVNDIYNRQIREIHEYSNHCVDYNTLE----- 215
QY 121 RPDISVLSNFKEMKMKVAKYKRGMAKMSLALFPTGPN-YPKQALKVQVROIF 179
DB 216 -----RLGFRSLAQMRYNQFRRELTLTVLDIVLPNDLSRLYPIQTSQLTREIYV 268
QY 180 APVIGIPGIGITSODSGPTFGSMRFDVKTYDQIDALROL-----MELYIQPLKSAVFW--- 231
DB 269 SPVSEFYGVV--NSGNIIIGTL-----TEQDIRPHLMDFNISMIMTYSNDRREHYWGL 321
QY 232 --IY-----ESDMKVRATVYND-----YIGKR 251
DB 322 EMTAVYFTGFAGAQVSFLVGTGRGESAPPLTVRSVNDGIYRILSAFYSAPFLGTVLGSR 381
QY 252 GSNNGAAMHMMSSDPSAIYTSALGAAGYAPNVGVRSYHSGSYTGMAAPANTNVAPEEF 311
DB 382 GEKFDPALNNISPPSTIYRH---PGTVDSLVS-----PPODNSVPP--- 421
QY 312 KYPGVKLHSVAYGLSKAPDAADSVMEGF--RPVLLENANQLTDTALQIPAEIGITDV 369
DB 422 -----HRGSHRLSHVTMRASSPIFHWTHRSATTNTIN--PMIIQIP-----L 464
QY 370 VPAFGRTPEEPINGODAIRIMESFTSGGFT-----YTVDSPQOKYKI 412
DB 465 VKAFNLH-----SGATVVR-----GPGFTGDIILRRNTGTGFADMRVNIITGPLEQRV 513

QY 413 IYRIANNLSASTVSLTYNNQTEFTDILNTSLDPNGVGVGYTLVEGP1IE----- 464
DB 514 RIRY-----ASTTDL-----QFFTRINGSVN-----QGNF-QRTNMRGNLBSGNFRTAG 558
QY 465 -----FSQGTNIFKLGSO---KGEPAIDSIIFSP 490
DB 559 FSTPFSFNAQSTFTLGTQAFNSNOEYIDRIEFVP 593
RESULT 11
US-08-291-368-4
Sequence 4, Application US/08291368
Patent No. 5686069
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5686069e1 Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,368
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/597,607
FILING DATE: 15-OCT-90
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MASO.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: Morrisson1
INDIVIDUAL ISOLATE: PS91C2
IMMEDIATE SOURCE:
LIBRARY: LAMBDAEM (TM) - 11 LIBRARY OF TERESA
LIBRARY: THOMPSON
CLONE: 91C2
US-08-291-368-4
Query Match 8.1%; Score 207.5; DB 1; Length 1168;
Best local Similarity 22.7%; Pred. No. 6.8e-11;
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;
QY 10 ITQFRLINNFYIAKL-QFSTNOSDLQ-----YFVL 41
DB 95 ITTRELADSYEYVLEALREWEMPNNAQLREDVRIRPANTDALITAINFTLSFEIP 154

QY 42 TLPLBAQCWHEMLMDKATTSVMGQQIDSOQLNGYAKELRLIKVYTNVNTYNOGLE 101
DB 155 LLSVYQANILHSLILKRAVSFGQGWGIDITVNNHVRLLNLHRYHECLDITYNOGLE 214
QY 102 LEKAKPLNYSDBEETLAGRPDISVLRNPFKEVKKWVAKYKGMASALSALAPPTF 161
DB 215 -----NLRGNTNQ---MSRFNQFRRLTLTVLDIYALFBNY 248
QY 162 GPN-YPKQALKVVSQRQIF-----APV-IGIPGITSQSGPFGSMRDVKTYYDID 212
DB 249 DARAPPIQTSSQL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVREPPLMD 298
QY 213 ALROLMELYIOLPSAYFW--IYESDMKVRATYVNDYIGKRGSTNGAAMHMSDPSAIY 270
DB 299 FMSNLF-VTAETVNSQTVGCHLVSRNTAGNPINFPYGVNFGALIW-IADEDDPRFPY 356
QY 271 TS-----ALGAAGYAPNVVGV-----YSHGSGYTKGN-----APANTVAAPF 309
DB 357 RLSDPVPVVRGFGDPHVLGLRGVFGQGTGNTNRTFRNSGTLDSLDEIPPODSGAPW 416
QY 310 E-----FKYPGYKLHVSAYGLSKAPDAADSVFGEFRPVLLNENAOILLTAL 358
DB 417 NDYSHVLNHTVFWPFG---EIASDSWRAP-----MFSWTH-RSADRNTIINPNIIT 465
QY 359 QIPA-----BIGITDV-VPAFRTEEPINGODAIRIWESFTSGRG-FTYTVDSPOKQY 410
DB 466 QIPAVKANLHSGSTVVGPGP-----TGADLRL-RVYTGFPADIRVNTITGLSOKY 516
QY 411 KIYRIANNLSASTVSLTYNNQTEFTDILNTSLDPNGVGVGYTLVEGP1IE----- 464
DB 517 RIRY-----ASTTDL-----QFFTRINGSVN-----QGNF-QRTNMRGNLBSGNFRT 561
QY 465 -----FSQGTNIFKLGSO---KGEPAIDSIIFSP 490
DB 562 AGFSTPFSFNAQSTFTLGTQAFNSNOEYIDRIEFVP 598
RESULT 12
US-08-962-190-4
Sequence 4, Application US/08962190
Patent No. 5985267
GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Sick, August J.
TITLE OF INVENTION: No. 5985267e1 Bacillus thuringiensis Isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/962,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/291,368
FILING DATE:
APPLICATION NUMBER: 07/597,607
FILING DATE: 15-OCT-90
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MASO.C1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: Morbisoni
INDIVIDUAL ISOLATE: PS91C2
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF TERESA
LIBRARY: THOMPSON
CLONE: 91C2
US-08-962-190-4

Query Match 8.1%; Score 207.5; DB 2; Length 1168;
Best Local Similarity 22.7%; Pred. No. 6.8e-11;
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

QY 10 ITQPRILNDNFIKTYAKL-QFSTNQSDDI-----YFVL 41
DB 95 ITTGLGLADSEYVLEALREWEENPNNAQLREVRIRPANTDDALITAINNFTLTSFEP 154
QY 42 TLPLRAQCVNHLMLLDATTSVWGQIDSQLNGYKALRLIKVYNDVNTYNOGLE 101
DB 155 LLSVYVQANLHLILRLDAVSFGQGWGIDATVNNHYNRLNLIRYEHCLDTYNOGLE 214
QY 102 LEKAKPLNYSDEEYLAQGRPDISVLSNFKKVMKKNVAKYKGMASLSLALPFTF 161
DB 215 -----NLRGNTNRQ---WSRFNGFRRLTLTVLDIYALFPNY 248
QY 162 GPN-YPKQALKVVSROIF-----APV-IGIPGITSQDSGPTFGSMRPDYKTYDQID 212
DB 249 DARAVPIQTSSQL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVRPPLMD 298
QY 213 ALRQMLLEYIOLPKSAVFW--IYESDMKVRATYNDYICKSGNTGAMHMSDPSAIY 270
DB 299 FMSNLF-VTAETVRQOTWGHVLSKRTAGNPIFPIYGVNPGGALN-IADEPRREFY 356
QY 271 TS-----ALGAAGYAPNVVGR---YSHGGSYTKM-----APANTNAYAPF 309
DB 357 RTLSDPVFVRGGFDPHYVLGLRGVGFQOTGTHNTRFRNSGTLSDLEIPQDSGAPW 416
QY 310 E-----FKYPGYKLSVSAVYGSKAPDAADSVMEGFRPVLLNEANQLITDAL 358
DB 417 NDYSHVNLHVTFFVRWFG---EIASGDSWRAP-----MFSWTH-RSADRTNINPNIT 465
QY 359 QIPA-----EIGITDV-VPAFGTEBPINGODAIRIMESFTSGFG-FTYVDSPOKXY 410
DB 466 QIPAKANHLMSGTSVVRGPGF-----TGGLDLR-RTNITGTADIRVANTGGLSORY 516
QY 411 KLIYRIANNLSASTVSLTYNNQTFETDLINTSLDPNGVAGNSYTLVEGPPIE----- 464
DB 517 RYRIYV-----ASTTDL-----QFETRLNGTSVN-----QGNF-QETNARGDLJESGNPRT 561
QY 465 -----FSQGTINIFKQSQ--KGEPAIDSIITSP 490
DB 562 AGFTSPFSFSNAQSTFTLGTQAFSNOEYVIRIEFVP 598

RESULT 13
PCT-US95-10310-4
Sequence 4, Application PC/TUS9510310
GENERAL INFORMATION:
APPLICANT: MYCOGEN CORPORATION
APPLICANT: STREET ADDRESS: 5501 Oberlin Drive
APPLICANT: CITY: San Diego

APPLICANT: STATE/PROVINCE: California
APPLICANT: COUNTRY: US
APPLICANT: POSTAL CODE/ZIP: 92121
APPLICANT: PHONE NUMBER: (619) 453-8030
APPLICANT: FAX NUMBER: (619) 453-6991
TITLE OF INVENTION: Protein Toxins Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanhik & Saliwanhik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10310
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/597,607
FILING DATE: 15-OCT-90
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanhik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA50.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904)375-8100
TELEFAX: (904)372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: BACILLUS THURINGIENSIS
STRAIN: Morbisoni
INDIVIDUAL ISOLATE: PS91C2
IMMEDIATE SOURCE:
LIBRARY: LAMBDAGEN (TM) - 11 LIBRARY OF TERESA
LIBRARY: THOMPSON
CLONE: 91C2
PCT-US95-10310-4

Query Match 8.1%; Score 207.5; DB 5; Length 1168;
Best Local Similarity 22.7%; Pred. No. 6.8e-11;
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

QY 10 ITQPRILNDNFIKTYAKL-QFSTNQSDDI-----YFVL 41
DB 95 ITTGLGLADSEYVLEALREWEENPNNAQLREVRIRPANTDDALITAINNFTLTSFEP 154
QY 42 TLPLRAQCVNHLMLLDATTSVWGQIDSQLNGYKALRLIKVYNDVNTYNOGLE 101
DB 155 LLSVYVQANLHLILRLDAVSFGQGWGIDATVNNHYNRLNLIRYEHCLDTYNOGLE 214
QY 102 LEKAKPLNYSDEEYLAQGRPDISVLSNFKKVMKKNVAKYKGMASLSLALPFTF 161
DB 215 -----NLRGNTNRQ---WSRFNGFRRLTLTVLDIYALFPNY 248
QY 162 GPN-YPKQALKVVSROIF-----APV-IGIPGITSQDSGPTFGSMRPDYKTYDQID 212
DB 249 DARAVPIQTSSQL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVRPPLMD 298

QY 213 ALRQIMELIYIOPKSAVFW--IYESDWKVRATVYNDYIGKSGNSGAAHMHSSDPSAIY 270
DB 299 FNNLSIF-VTAETVRS-----QIVWGGHLYSSRNTAGRIINFPBGVFNPGGAIWIADSD 351
QY 271 TS-----ALGAGYAPNVVGR---YSHGGSYTKGM-----APANTYAYAF 309
DB 357 RLSDPVPFRGGPBDPHVYLGLRGVGFQQTGNNHTRTFNNSGTSIDSLDEIPQDMSGANW 416
QY 310 E-----FKYPGYKLHSVSAVGLSKAPDAADSVWFGFRVLLNEANQLLDTAL 358
DB 417 NDYSHVHNHTVFRWPG---EISGDSWRAP-----MFSWTH-RSADRTMIINPNT 465
QY 359 QIPA-----EIGITDV-VPAGRTTEPINGODAIRIMESFTSGEG-FITYVDSPOKXY 410
DB 466 QIPAYKANHLHSGSTVVRGPGF-----TGDDLK-RTNVTGETFADIRVNTIGLSORX 516
QY 411 KIYRIANNLSASTVSLTYNNQTFETDIINTSLDPNGRGVNGSYTLVEGPPIE----- 464
DB 517 RVRIRY-----ASTIDL-----QFTRINGTSVN---QGNF-QRTMNRGDMLESQNFRT 561
QY 465 -----FSOGTNIYKLGSO--KGEPAIDSIIFSP 490
DB 562 AGSTPFSFMSNAQSTFTLGTQAFSNQEVYIDRIEFVP 598

RESULT 14
US-09-178-252-4
; Sequence 4, Application US/09178252
; Patent No. 6218188
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2
; CURRENT APPLICATION NUMBER: US/09/178,252
; PRIOR FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; EARLIER APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-178-252-4

Query Match 7.8%; Score 200; DB 3; Length 605;
Best Local Similarity 22.0%; Pred. No. 1.3e-10;
Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;
QY 10 ITQFRIANDNFIKYIAKL-QFSTNOSDLO-----YVYL 41
DB 95 ITTLRLASDYEIYIEALREWEANPNNAQLREDVRIRPANTDDALITAINNFTLTSFEIP 154
QY 42 TLPLRAQACVMHMLLKDATTSVWGQIDISQOLNGYKAEILIRLIKVTYNDVNTVYNGGLE 101
DB 155 LISVYQAAANHLSLIRDAVSPGQGWGLDIATVNNHNYRLINLIHRYTKHCLDITYNGGLE 214
QY 102 LEKAPLNVSDPEEYLAQGRPDISVLRSNFKEVWKNVAKYKGGMAWSALSLAALPFTF 161
DB 215 -----NLRGNTNRQ---WARFNQFRRLDTLTVLIDIVALFBNY 248
QY 162 G-PNYPKQALKVVSROIF-----APV-IGIPGIGTSQDSGPTGSRFRDYKTYDQID 212
DB 249 DVRTPIQTSQOL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVRPPLHMD 298
QY 213 ALRQIMELIYIOPKSAVFWIYESDWKVRATVYNDYIGKSGS-----NTGAAMHMHSSD 265

DB 299 FNNLSIF-VTAETVRS-----QIVWGGHLYSSRNTAGRIINFPBGVFNPGGAIWIADSD 351
QY 266 PSAIYTS-----ALGAGYAPNVVGR---YSHGGSYTKGM-----APANTN 304
DB 352 PRPFYRLSDPVPFRGGPBDPHVYLGLRGVAFQQTGNNHTRTFNNSGTSIDSLDEIPQDN 411
QY 305 AYAPE-----FKYPGYKLHSVSAVGLSKAPDAADSVWFGFRVLLNEANQLL 353
DB 412 SGAPMNDYSHVHNHTVFRWPG---EISGDSWRAP-----MFSWTH-RSADRTMTID 460
QY 354 TDTALQIP-----AIGITDV-VPAGRTTEPINGODAIRIMESFTSGEGFTYTV----- 402
DB 461 PERIQIPLVKAHNLQSGTIVVRGPGF-----TGDDLK-----RTSGGFATYIVNIN 509
QY 403 -DSPQKQYKIIYRIANNLSASTVSLTYNNQTFETDIINTSLDPNGRGVNGSY----- 455
DB 510 GOLPQRYARARIRYASTNL---RIYVTVAGSRIFAGCFNKMTD-TGDLPLTFQSFSEYATIN 565
QY 456 TLVEGPPIE--FSOGTNIYKLGSOKEPAIDSIIFSPV 491
DB 566 TATTFEMSQSFVAGADTFSSGN---EYIDREFELIPV 600

RESULT 15
US-09-826-660-4
; Sequence 4, Application US/09826660
; Patent No. 6673990
; GENERAL INFORMATION:
; APPLICANT: Cardineau, Guy A.
; APPLICANT: Stelman, Steven J.
; APPLICANT: Narva, Kenneth E.
; TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
; FILE REFERENCE: MA-714XC2D1
; CURRENT APPLICATION NUMBER: US/09/826,660
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/178,252
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/065,215
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/076,445
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene
US-09-826-660-4

Query Match 7.8%; Score 200; DB 4; Length 605;
Best Local Similarity 22.0%; Pred. No. 1.3e-10;
Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;
QY 10 ITQFRIANDNFIKYIAKL-QFSTNOSDLO-----YVYL 41
DB 95 ITTLRLASDYEIYIEALREWEANPNNAQLREDVRIRPANTDDALITAINNFTLTSFEIP 154
QY 42 TLPLRAQACVMHMLLKDATTSVWGQIDISQOLNGYKAEILIRLIKVTYNDVNTVYNGGLE 101
DB 155 LISVYQAAANHLSLIRDAVSPGQGWGLDIATVNNHNYRLINLIHRYTKHCLDITYNGGLE 214
QY 102 LEKAPLNVSDPEEYLAQGRPDISVLRSNFKEVWKNVAKYKGGMAWSALSLAALPFTF 161
DB 215 -----NLRGNTNRQ---WARFNQFRRLDTLTVLIDIVALFBNY 248
QY 162 G-PNYPKQALKVVSROIF-----APV-IGIPGIGTSQDSGPTGSRFRDYKTYDQID 212
DB 249 DVRTPIQTSQOL-TREIYTSVIEDSPVSANIPNG-----FNRAEFGVRPPLHMD 298
QY 213 ALRQIMELIYIOPKSAVFWIYESDWKVRATVYNDYIGKSGS-----NTGAAMHMHSSD 265

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Db 299 FMNSLF-VTAETVRS-----QVWGCHLVSSRNTAGNRINFPsyGVNPGAIWIADDE 351
Qy 266 PSAIYTS-----ALGAGYAPNVVGV-----YSHGGSYTKGM-----APANTN 304
Db 352 PRPFYRTLSDFVFRGFGFNPHYVLGLRGVAFQOTGNTNTRIFPNSGTIISLDEIIPODN 411
Qy 305 AYAPPE-----FKYPGYKLHSVAYGLSKAPDAADVMEGFPPVLLNEANQIL 353
Db 412 SGAPMNDYSHVLNHTFVRWPG-----EISGDSWRAP-----MFSWTH-RSATPTNTID 460
Qy 354 TDTALQIP-----AEIGITDV-VPAFGRTBEPINGODAIRIWESFTSGFGFTYTV----- 402
Db 461 PERITQIPLVKAHTLOSSTVVRGPGF-----TGDIILR-----RTSGPFAYYTIVIN 509
Qy 403 -DSPQKXKXIIYRIANNLSASTVSLTYNNQTFFTDILNTSLDPNGVGNVGSY----- 455
Db 510 GOLPORRYRIRRYASTNL--RIYTVAGERIFAGQFNKTWD-TGDPITFOSFSYATIN 565
Qy 456 TLVEGPPIE--FSOGTNIIFKLGSQKGEFAIDSIIIFSPV 491
Db 566 TAFTEPMQSSTVVGADTFSSGN--EYIDRFELIPV 600

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Search completed: October 19, 2005, 20:19:21
 Job time : 46 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:04:21 ; Search time 166 Seconds
(without alignments)
1146.302 Million cell updates/sec

Title: US-10-756-778-8
Perfect score: 2560
Sequence: 1 IAEPPSTGVITQFRILNDNF.....KLSQKGEFAIDSIIFSPV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	9.0	825	ADP43080	Adf43080 Bacillus
2	228.5	8.9	1138	AAR06461	Aar06461 BtPGS1245
3	228.5	8.9	1138	ADR89429	Adr89429 cry7Aa.1
4	227.5	8.9	1152	AAB84630	Aab84630 Amino aci
5	225.5	8.8	1138	AAR37213	Aar37213 B.c. toxi
6	224.5	8.8	1138	AAR46225	Aar46225 Bacillus
7	223.5	8.7	1169	AAR96126	Aar96126 Bacillus
8	222.5	8.7	1138	AAR46226	Aar46226 Bacillus
9	220.5	8.6	1138	AAR37214	Aar37214 B.c. toxi
10	214	8.4	1186	AAU00419	Aau00419 Bacillus
11	210.5	8.2	1167	AAR54073	Aar54073 CryET4. 2
12	210.5	8.2	1167	AAW35258	Aaw35258 Bacillus
13	210.5	8.2	1167	AAW17700	Aaw17700 CryET4. 3
14	210.5	8.2	1167	AAW87632	Aaw87632 CryET4 pr
15	210.5	8.2	1167	AAI30922	Aay30922 B. thurin
16	207.5	8.1	1168	AAR89493	Aar89493 CryIF cia
17	207	8.1	1168	ADR89437	Adr89437 Cry39Aa.
18	203	7.9	1174	AAR94916	Aar94916 Native Cr
19	201	7.9	1157	AAW84581	Aaw84581 Amino aci
20	201	7.9	1157	AAW84583	Aaw84583 Amino aci
21	201	7.9	1157	AAW84591	Aaw84591 Amino aci
22	200	7.8	605	AAI16791	Aay16791 Truncated
23	200	7.8	605	AAU00532	Aau00532 Truncated
24	200	7.8	718	AAW61024	Aaw61024 Chimeric
25	200	7.8	1148	AAR84733	Aar84733 CryIF/cry

26	200	7.8	1148	2	AAR84731	Aar84731 CryIF/cry
27	200	7.8	1148	2	AAR94907	Aar94907 CryIF/cry
28	200	7.8	1148	2	AAW76709	Aaw76709 Plasmid p
29	200	7.8	1148	2	AAW76715	Aaw76715 Consensus
30	200	7.8	1148	2	AAW76718	Aaw76718 Alternati
31	200	7.8	1148	2	AAW76717	Aaw76717 Alternati
32	200	7.8	1148	2	AAW76707	Aaw76707 Plasmid p
33	200	7.8	1148	2	AAW16790	Aay16790 Plasmid p
34	200	7.8	1148	4	AAU00531	Aau00531 CryIF/cry
35	200	7.8	1157	2	AAW84569	Aaw84569 Amino aci
36	200	7.8	1174	2	AAR10131	Aar10131 Lepidopte
37	200	7.8	1174	2	AAR14856	Aar14856 CryIF pro
38	200	7.8	1174	2	AAR39754	Aar39754 Delta end
39	200	7.8	1174	2	AAR84732	Aar84732 CryIF/436
40	200	7.8	1174	2	AAR84735	Aar84735 CryIF/436
41	200	7.8	1174	2	AAR94908	Aar94908 CryIF/436
42	200	7.8	1174	2	AAR94914	Aar94914 CryIF tox
43	200	7.8	1174	2	AAW76712	Aaw76712 B. thurin
44	200	7.8	1174	2	AAW76710	Aaw76710 Plasmid p
45	200	7.8	1174	2	AAW76708	Aaw76708 Plasmid p

ALIGNMENTS

RESULT 1	ADP43080	ADP43080 standard; protein, 825 AA.
ID	ADP43080	
XX	ADP43080;	
AC	ADP43080;	
XX	ADP43080;	
DT	12-FEB-2004 (first entry)	
DE	Bacillus thuringiensis toxin protein sequence.	
XX	cell recognition; cell-damaging; cytostatic; anticancer;	
KW	cancer affected cell.	
XX	Bacillus thuringiensis.	
OS	Bacillus thuringiensis.	
XX	JP200310277-A.	
FN	05-NOV-2003.	
PD	30-APR-2002; 2002JP-00129344.	
XX	30-APR-2002; 2002JP-00129344.	
PF	30-APR-2002; 2002JP-00129344.	
XX	30-APR-2002; 2002JP-00129344.	
PR	30-APR-2002; 2002JP-00129344.	
XX	(FUKU-) FUKUOKA KEN.	
PA	(FUKU-) FUKUOKA KEN.	
XX	WPI, 2004-027149/03.	
DR	N-PSDB; ADP43079.	
XX	Novel polynucleotide encoding a 88 kDa protein having cell	
PT	recognizing/cell damaging activity useful as an anticancer agent.	
XX	Claim 15; SEQ ID NO 2; 26pp; Japanese.	
PS	This invention relates to a novel nucleotide with specific cell	
CC	recognition and cell-damaging activity. The invention may be useful for	
CC	the development of compositions with a cytostatic (anticancer) activity	
CC	which damages cancer affected cells.	
XX	Sequence 825 AA;	
SQ	Sequence 825 AA;	
Query Match	9.0%; Score 230; DB 8; Length 825;	
Best Local Similarity	21.0%; Pred. No. 1.8e-11;	
Matches	120; Conservative 90; Mismatches 213; Indels 148; Gaps 24;	
QY	9 VITGRRIN---DNFIKIALQFSTNOSDQYPLTIPLAQAQWHTIMLKQATT--S 63	
DB	164 VLTEPRVNGHGFENSMPSFAVRNFEVN-----LLPVYAEANHLILLIRDAVKRGE 214	

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QY 64 VMGQID--SQQLNGYKAEILRLIKYTNVDVNTTNOGLEKAKPLNTSDPE-----EY 116
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 215 GWMSTDPGEAREDDMYR-RLRSRETEIYTDHCWVTYNOGLQAKSLQANVSDSRYPWTQY 273
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 117 LQAGRPDISVLSNFEWKKMKVAKYKKGMMASLSLALPTPEPNPKQALKVQSR 176
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 274 NQSGGFSYBEAAGEYRGTEMMNLVNAFRKDMTLVLIDIAQFPPTYPDGLYSRPVSELR 333
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 177 QIFAPVIGIPGIGITSQDSGPTFGSMRFVKTVDQID---ALROL-----MELYIOP 224
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 334 EYVTDIRG-----TWRSQANLITIDALENRVGSRLQQLFTWLTMEKRYIYN 381
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 225 LKSAFWIYES----DMKVRATYVND-YIGKSGNTGA-----WH-----260
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 382 TGSITSYTHGDLNVGLEKKIRKTNDDQWLPLEGQNTSYTRIDRPGIELGKVVYVYARQ 441
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 261 -----MM-SDPSAITYTSALGAGYAPNVVGRYHGGSYTGGMARPAATNAYAPPE 310
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 442 QMFETRLIQLMANTDVLISNAGTVGNEFWVRDVPDRNLYASTRNHFTENHRLSWIKPE 501
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 311 -----FKYPGYKLHSVSAVGLSKAPDAADSVMFGRPVLLLENANQLLTDALQIPA- 362
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 502 PYRDNCFAMPGYKQSLALFGWTNNSVDLNNIISQYR-----ITQIPAV 546
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 363 ---BIGITDVPAFGRTPEEPINGODAIRIMESFTSGFGFTYTVDSPOKOKYIIRIAN 418
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 547 KAYMNRGAFSVIRGPST-----GGNLVQL-----GTGGEVSVKVRPEQTSQDWYRARI 595
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 419 NLASAT-----VSLTYN-NOTFFTDILNTSLDPNGVRGNVGSYTIIVEGPII 463
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 596 RLAASRGKLANVKYVSSIHASVTYDYNMTM-----SSSTQGTVNSFOYLD--VY 643
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 464 EFSOGTNIIFKL--GSQKGEPAIDSIIFSPV 491
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 644 NERLAEPFEVWLTMESGSPWIDKIEFIPL 674
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 2
AAR06461
ID AAR06461 standard; protein; 1138 AA.
XX
AC AAR06461;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 03-JAN-1991 (first entry)
XX
DE BtPGS1245 protoxin.
XX
XX Toxin; crystal; insecticide.
XX
XX Bacillus thuringiensis; strain PGs1245.
OS
FH Key location/Qualifiers
FT Protein /label= BtPGS1245
XX
XX EP382990-A.
XX
XX 22-AUG-1990.
XX
XX 15-FEB-1989; 89EP-00400428.
XX
XX 15-FEB-1989; 89EP-00400428.
XX
XX 15-FEB-1989; 89EP-00400428.
XX
XX (PLBZ ) PLANT GENETIC SYSTEMS NV.
XX
XX Peferoen M, Lambert B, Joos H;
XX
XX WPI, 1990-255362/34.
XX
XX N-PSDB; AAQ05680.
XX
XX New Bacillus thuringiensis strains - producing toxin active against
PT

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PT Coleoptera.
XX
XX Claim 2; Fig 2; 30pp; English.
XX
CC The BtPGS1245 strain was isolated from grain dust and was deposited at
CC the DSM (19/1/1989) under Acc. No. 5132. The protoxin (129 kD) can be
CC digested with trypsin to produce the mature protein (66 kD). The proteins
CC formed during sporulation are packaged in bipyramidal crystals. Plants
CC contg. the gene encoding the toxin are resistant to Coleoptera pests
CC while the crystals are useful as insecticides. The gene can also be
CC truncated and used to produce chimaeric genes together with the bPGS1208
CC gene (AAQ05679). See also AAR06460. (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 1138 AA;

Query Match      8.9%; Score 228.5; DB 2; Length 1138;
Best Local Similarity 22.4%; Pred. No. 4.1e-11;
Matches 124; Conservative 70; Mismatches 216; Indels 143; Gaps 23;

QY 9 VITOPRIINDNFIKXIAKLOFTNQSDIQ-YPVLTLPRAQACVWHMLMDATP--SVW 65
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 157 VATERRIITLSLF-----EFSMBSFKYTGVEIPLITVYAQANLHLALRDSITYGDKW 209
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 66 G--QQIDSQQLNGYKAEILRLIKYTNVDVNTTNOGLEKAKPLNTSDPEEYIQAQRPD 123
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 210 GFTQNNIEBNYNRQK-----KRISEYSDHCTKWNSGLS-----243
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 124 ISVLSNKEVKKMKVAKYKKGMMASLSLALPPTGPNYPKQALKVQSRQIFAVI 183
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 244 ---RLNSTYEQWLNVRFRREMILMALDLVAVFPFHPDRYSMETSTOLTREYTTDPV 299
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 184 GIPGIGITSQDSGPTFGSM-RFDVKTYPDIDALROLMELYIQPLKSAFWIYESDVKVRAT 242
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 300 SL--SISNPDIQGESQMENTAIRPHLVYLDLDEL-----YITTSKTKASH 344
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 243 YVNDYIGKRGSGNTGAMHMS-----SDPSAITYSAL--GAGYAPNVVGRYSHGG 292
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 345 EIQPDL-----FYMSAHKVSFKKSEQSNLYTTGIGKTSGYISS--GAVSFHGN 391
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 293 SYTKGMAPANTNAYAPPEFKTP--GYKLHSVSAVGL-----SKAPDAADSVW 337
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 392 DIYRTLA-----APSVVVPYTONYGEQVEFYGAVGHVHRGDNKYDLTYPSIDQLP 444
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 338 FGFRPVLLLENANQLLTDALQIPAEIGITDVVPAFGRT-----EPINGODAI 386
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 445 PDGEPY-HEKYYTRKCHATAIFKSTPYDNAATTIPFSWTHSAEYVNRYPNKIKTIPAV 503
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 387 RIWE-----SFTSGFGFT-----YTVDSPOKOKYKIIVRIANNLSAST 424
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 504 KMYKLDDESTVVKGGFTGDLVKRGSTGYIGDIKATVNSPLSQYRVVRVAVATVSGQF 563
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 425 VSLTYNNOTFFTDILNT-SLDPNGVRGNVGSYTLVE-GPIIEFSOGTNIIFKLG----SQK 478
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 564 NVYINDKLTITQKQNTVEYTIQEGKDLTYGSGFYIEVSTTIOFPDEHPKITLHSDLSNN 623
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 479 GEPALDSIIFSPV 491
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 624 SSFYVDSIEFIIPV 636
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 3
ADR89429
ID ADR89429 standard; protein; 1138 AA.
XX
AC ADR89429;
XX
XX 18-NOV-2004 (first entry)
XX
XX cry7Aa.
XX
XX delta-endotoxin; delta-endotoxin associate polypeptide;
XX
XX expression cassette; transformation; transgenic; plant; bacteria;
KW

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	Best Local Similarity	24.4%	Pred. No. 5.2e-11;	
	Matches	132;	Conservative	71; Mismatches 223; Indels 115; Gaps 30;
Qy	9	VITQFRILNDIFIKIYAKIQFSTNSDQLQYPLTLPLEPAQACVMHMLLKDATY--SVWG	66	
Db	168	LFNFRTTLDISLPTQMP--SFQTGSGSQNVAVPLATVVAQAANLHLLLKDEIYGARKG	225	
Qy	67	QOIDSQQLNGYKAEILIRLIKVTYNDVNTTYNGLELEKAKPLINSDPEEYLOAGRPDISV	126	
Db	226	--LNQNIQINSFHTRQOERTQYTYTTHCVTTNTGLDR-----	259	
Qy	127	LRSNFKEVMKNNKVAKYRGMAASLSIALAFLPTTG--PNYPKQALKVQVSROIFA--PVIG	184	
Db	260	LRGTNTE--SMLNHYRFRREMTLMAMDVLALPEYVNVARQYPGANPOL--TREIYNDPIYV	316	
Qy	185	IP---GGITSQDSGP--TFGSMR---FDVKTQOIDALRQLMELYIQPLKSAY--FWI	232	
Db	317	NPPANQIGICRKGNNPNTTFSLEENAFIRPHLPRLNRLTISRNRYYAPPTNSLYDYV--	375	
Qy	233	YESDMKVRATYVND-----YIGKRGSNY-----GAAMHWSDDPSA1YTSALGAAGY	279	
Db	376	--SGHTTQSOYANNPTTYETSYGQITSNTRLFNNTNGA-----NAIDSRANFGNL	424	
Qy	280	APNVGVGVYSH---GGSYTKGMAPANT-----NATAPEEFKPYGKLHSVSAYGSKAPD	331	
Db	425	YANYGVGSYLVNIFPTGVMSSEITSAPNTCMODLTTEELPLVNNNNLISHVFLFENYTO	484	
Qy	332	AADSVMFSPRPVLL-----ENEAQOLLTDTAL-QIPAEIGITDVNPAF-----GRT--EEP	379	
Db	485	GGPLATGVFVPIYVTRQDVDPNNIITPRRIQIP-----VKAIVELSSGATVYKGG	537	
Qy	380	INGODAIRIWESFTSGFG--FTYVYDPSPOKOKIYIRIANNLSAS---TVSLTYNNQTFE	435	
Db	538	FTGGGVIR--RINTGGFGARIVSVGPLQRIRIRFRAVSTIDPDPFVIRGGTTINNPRF	595	
Qy	436	TDILNTSLDPNGVRCNNGSYTLVSGPI--IESQGNINFEKLSQ---KGEFAIDSIIFSP	490	
Db	596	TRTMV-----RGQESRYESYRTVEFTTPEFNFTQOSODIIRTSIQGLSGNGEVVLDRIELIP	650	
Qy	491	V 491		
Db	651	V 651		
RESULT 5				
AAR37213				
ID	AAR37213 standard; protein; 1138 AA.			
XX	AAR37213;			
XX	24-OCT-2003	(revised)		
AC	25-MAR-2003	(revised)		
DT	14-SEP-1993	(first entry)		
DE	B.t. toxin HD511.			
KW	Coleopterian pests: Bacillus thuringiensis; insecticide; transgenic;			
XX	plant; pepticide; Colorado potato beetle.			
OS	Bacillus thuringiensis; strain HD511.			
XX	W09308693-A1.			
PN	13-MAY-1993.			
PD	06-NOV-1992;	92WO-US009510.		
XX	06-NOV-1991;	91US-00788638.		
XX	(MYCO) MYCOGEN CORP.			
PA	Payne JM, Fu JM;			
XX				

DR	WP1; 1993-167285/20.
DR	N-PSDBj; AAQ41744.
XX	
PT	Control of coleopterian insect pests using bacillus thuringiensis - using
PT	strains Bt HD 511, HD 867 or HD 1011 or their toxins or nucleotide
PT	sequences.
XX	
PS	Claim 9; Page 15-18; 29pp; English.
XX	
CC	The DNA sequence encoding Bacillus thuringiensis strain HD 511 toxin may
CC	be used in an insecticide/pesticide for treatment of Coleopterian pests,
CC	esp. the Colorado potato beetle. Strain HD511 and recombinant cells
CC	contg. the gene encoding the toxin may be treated by chemical or physical
CC	means to prolong the pesticidal activity of the cells, the treated cells
CC	acting as a protective coating for the pesticidal toxin, which becomes
CC	available upon ingestion by a target insect. The compen. may be applied
CC	to the environment of the coleoptera, e.g. plants, soil or water, by
CC	spraying, dusting, etc. See also AAK37214. (Updated on 25-MAR-2003 to
CC	correct FN field.) (Updated on 24-OCT-2003 to standardise OS field)
XX	
SQ	Sequence 1138 AA;
Query Match	8.8%; Score 225.5; DB 2; Length 1138;
Best Local Similarity	22.5%; Pred. No.7.8e-11;
Matches 126;	Conservative 75; Mismatches 207; Indels 151; Gaps 25
OY	7 TGVITPFIIDNFNFIKYIAKIQFSTNSDLDYPLTTLPLRAQACVHMLLKDATT--SV 64
Dd	155 TRVIDRRPIILDALFEYSMPFRVA-----GYEIPLTLYVQAANHLALRDSLYGDK 208
OY	65 WG--QQIDSQOLNGYKAELIRLIKVTNDVNTTYNQGLELEKAPFLANSDEPEYLQAGRP 122
Dd	209 WGFQNNEENRYNRK----KHISEYNHCVKWYNSGLS----- 243
OY	123 DISLRSNFKKVMKMKYAKKRCGMASLSLALFPFGFNYPKQALKVQSRIQIPAV 182
Dd	244 -----RLNGSTGEOWINMYRRREMILMVLDIAAVFPIYDPMYSMETSTOLTREVIYDP 298
OY	183 IGIPOGATISDOSGPFGFSGRFDV-KTYDOIIDLRLQLMELYIOPLK-----SAYFW 231
Dd	299 ISL--SISNPICIGFSQMEHTARTPLUV---YLDELIIYTTSKKYAFSHIEIOPDLTYW 353
OY	232 -IYESDWKVARTYVNDYIGKRGSNTGAAMHMSSDSPSAITYSAL--GAAGYAAPNVVGVR 288
Dd	354 CVHKVSFK-----KSQSNLYTTGIVGKTISGY--ISSGAY 386
OY	289 SHGS--YTKGMAFA-----NTNAVAPREFPYCYKLH---SYSAYGLSKAPDAADSYM 337
Dd	387 SFRNDIIRTLAAPSVVVPYTOVYGVEQVFGYGGVHYRGDNKDYLY--DSIDOLP 444
OY	338 FGPRPVLLBNANOLDPTALQIPAEIGITDVPAFGTE-----EPINGODAI 386
Dd	445 PDGETI-HEKTHRLCAATAISKSTPDYDNAATIPIFSWTHRSAEYRNRIYPNKIKKIPAV 503
OY	387 RIWE-----FTSGFGFT-----YTVDSFOKOKYKIIVIANNLASA-- 422
Dd	504 KMYLDDLDSLTYVKGEGFTGCDLVKRGANGYIGDIKATVNSLSQKXRVAVAYSVSGLF 563
OY	423 ----STVSLTYNNQTFFPTDILTNSLSDENVRGVNGSYTLVE-GPIIEFSOGTNIFKLG- 475
Dd	564 NVFINDEIALQKNFOSIVETI-----GEGKDLTVGSGFYEVSTTIQIPVENHPKITLIHL 617
OY	476 ---SOKGFALDISIIFSPV 491
Dd	618 NHLSNSPFYVDSEIFIV 636
RESULT 6	
ID	AAR46225
AC	AAR46225 standard; protein; 1138 AA.
XX	
XX	AAR46225;


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Oy 368 IWE-----STSGGPF-----YTDSPOKCKIIVYIANNLSA---422
Db 505 MYKDLUDLSTVYKGGPGFTGGDLVYKRGSIYIGDIKATYNSLSQKTYRRVAYAISVSGLFN 564
Oy 423 ----STVSLTYNNQTFPTDILNLSLDENGVRGNVGSYTLVE-GEIIFPSQGTNIYFKLG--475
Db 565 VFINDLALQKNFGSTVETI-----GEGDLTFYGSFGYIEVSTTIGFPMHFKITLHLN 618
Oy 476 --SQKEFPAIDSIIFSPV 491
Db 619 HLSNNSFFYVDSIEFIPV 636

RESULT 7
AAR96126
AAR96126 standard; protein; 1169 AA.
AAR96126;
AAR96126;
16-OCT-2003 (revised)
28-OCT-1996 (first entry)
Bacillus thuringiensis crystal protein.
Bacillus thuringiensis; crystal protein; delta toxin; insecticide;
Lepidoptera; Coleoptera; crop protection; rice; wheat; beans; tea;
Sugarcane; cauliflower; cabbage; apple; citrus fruit.
Bacillus thuringiensis; var. japonensis.
strain N141.
EP11834-A2.
15-MAY-1996.
13-OCT-1995; 95EP-00307293.
14-OCT-1994; 94JP-00276082.
(NISC ) NISSAN CHEM IND LTD.
Iizuka T, Tagawa M, Arai S, Mizuki M, Miyake T;
NPI: 1996-232099/24. ~
N-PSDB; MAT27148.
B. thuringiensis var japonensis strain N141 insecticidal crystal protein
used to protect plant from damage by pest, partit, lepidoptera or
coleoptera insects.
Claim 3; Page 12-16; 20pp; English.
The crystal protein is toxic to insects of the order Lepidoptera or
Coleoptera, it is therefore useful in the protection of crops which are
subject to infestation with lepidopterous or coleopterous insect pests.
The crystal protein is formulated into a spray so that the protein agent
is applied to crops at an amount of 0.1 to 5kg per hectare. Plants to be
protected by such methods include vegetables such as cauliflower and
cabbage, fruit trees such as citrus and apples, grains such as rice,
wheat and beans and industrial crops such as tea and sugarcane. (Updated
on 16-OCT-2003 to standardise OS field)

Sequence 1169 AA:
Query Match 8.7%; Score 223.5; DB 2; Length 1169;
Best Local Similarity 22.3%; Pred. No. 1.2e-10;
Matches 130; Conserve 78; Mismatches 192; Indels 183; Gaps 30;

Oy 9 VITQRIINDFIYIAKLPSTNQSDLOYVLTLPARAQCVHMLMDATP--SVWG 66
Db 168 VSGQFNILDSLTFQFMP--STGSGPGSQGNVATILLPVYAQAANHLLILMDADITYGARWG 225

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QY 67 QOIDSQQLNGYKAEILRLIKVTNDVNTTYNOGLELEKAKPLNYSDBEYLQAGRPDISV 126
DB 226 --LNQTOIDQFHSRQOSLTQTNTNHCVTAYNDGL-----AE 259
QY 127 LRSNFEWKKMKVAKYKRGMAAMSLALAPPTGPNYPKQALKVQSRQIFAPYIGI- 185
DB 260 LRGTTAAE--SMFKYNDYKREMTLTAMDVALPYYNLKROYPDGTNPQLTRREYTDPIAD 317
QY 186 ----PGGITSQ-----DSGPTF-GSMKRPDV-----KTYDQIDALRQIMELYIOPUK 226
DB 318 PLEQF---TTQCRSMYINPAPFRNHLNFSVLENSLIRPHLPERLSNLQILVN--YQTNIG 372
QY 227 SA-----YFWYIESDMKVRA--TYVNDYIGKR-----GSNTGAAWH 260
DB 373 SAMRGSRRVHYHSHSIIQEKSYGLSDPYGANINQNDYIYQISQVSNFASPVSSYS 432
QY 261 MMSDPSAIYTSN--LGAAGVAPNVGV-----RYSHGGSV 294
DB 433 VMDTN---FYLSSGVSGISGYTQOGIPAVCLQQRNSTDBELPSLANEGDIIIRNYSIRLSH 489
QY 295 -----TKGMAPANTNAYAPPEFYKPGYKLHSVASAYGLSKAPDAADSVMEGFEPVLE 346
DB 490 ITQYRFQATQSGSPSTVSANLP-----TCVWTHRDVDD 523
QY 347 N--EANOULTDTALQIP-----AETGIDTV--PAFGRTBEPIINGODAIRMESFTSGG 397
DB 524 NITTAQI-----TOLPLVAYELSSGATVVGKPGF-----TGQDVIR--RTNNGGFG 569
QY 398 -FTYVDSPOKOKYKIIYRIANNLSAS--TVSLTYNNQTFPDILNTSLDPNGVAGNGY 453
DB 570 AIRVSTGELTQYRIRFRKASTIIDDFPYTRGCTIINFRFRYMA-----RGQSRYE 624
QY 454 SYTLVEGPI-IEFSQGTNIFKLGSO---KGEFAIDSIIFSPV 491
DB 625 SYRTVEFTTPEMFTQSDIIRTSIQGLSGNGEYVLDRIEIPV 667

RESULT 8
AAR46226
ID AAR46226 standard; protein; 1138 AA.
XX
AC AAR46226;
XX
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 07-JUL-1994 (first entry)
XX
DE Bacillus thuringiensis toxin HD867.
XX
KW Bacillus thuringiensis; B.t; Coleoptera; insect pest; toxin; HD511;
KW HD867; biological control agent; crystal protein; insect resistance.
XX
OS Bacillus thuringiensis; kumamotoensis.
XX
PN US5286486-A.
XX
PD 15-FEB-1994.
XX
PF 06-NOV-1992; 92US-00973320.
XX
PR 06-NOV-1991; 91US-00786638.
XX
PA (MYCO ) MYCOGEN CORP.
XX
PI Fu JM, Payne JM;
XX
DR WPI; 1994-057203/07.
XX
DR N-PSDB; AAQ56922.
XX
PT Nucleotide sequence encoding Bacillus thuringiensis toxin active against
PT coleopteran pests - used to produce transformed host cells with
PT insecticidal activity.
XX
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PS Disclosure; Col 23-24 to 29-30; 16pp; English.
XX
XX Toxin HD511 (AAR46225) from B. thuringiensis dakota serotype 15 and toxin
CC HD867 (AAR46226) from B. thuringiensis kumamotoensis serotype 18 are
CC crystal proteins that can be expressed in microbial hosts for use in the
CC biological control of coleopteran pests, e.g. Colorado potato beetle, or
CC in plants to improve insect-resistance. They are encoded by sequences
CC AAQ56921-22. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16
CC -OCT-2003 to standardise OS field)
XX
SQ Sequence 1138 AA;

Query Match 8.7%; Score 222.5; DB 2; Length 1138;
Best Local Similarity 22.4%; Pred. No. 1.5e-10;
Matches 125; Conservative 77; Mismatches 207; Indels 149; Gaps 25;

QY 7 TGVITQPRILNDNPKFYIAKLOFSTNGSDLOYVLTLLPRAQACMHLMLKDATTSWNG 66
DB 155 TRVIDRFILDLNLFSTNPSFRVA-----GEIPLLVYQDANLHLALRDSI--LYG 206
QY 67 QOIDSQQLN--GYKAEILRLIKVTNDVNTTYNOGLELEKAKPLNYSDBEYLQAGRPD 123
DB 207 DKMEFTQNNIENYNRQK-KHISEYSHCVKYNNGLS----- 243
QY 124 ISVLRSNFEWKKMKVAKYKRGMAAMSLALAPPTGPNYPKQALKVQSRQIFAPYI 183
DB 244 ----RLNSGYEQMINYRFRREMTLWDLDAVFPYIDPNYSMETSTQLTRREYTDPI 299
QY 184 GIPGITSQDSGPTFGSM-REPDVKTVDQIDALRQIMELYIOPKLSAYFWYIESDMKVRA 242
DB 300 SL--SISNPGIGPSTQOMENTAIRPHLVYIDEL-----YIYSKYKARSH 344
QY 243 YVNDYIGKRGNTGAMHMS-----SDPSAIYTSAL--GAAGVAPNVGVARYSHGG 292
DB 345 RIQPDL-----FYMSAHKVSFKQSEBSNLVTIGIYKTSGYISS-----G 384
QY 293 SYT-KGMAPANTNAYAPPEFYKPGYKLHSVASAYGL-----SKAPDAADV 336
DB 385 AYSFPGNDIYRTLA-APSVVVYPTQNTGVEQVEFYGVKHYDVRGDNKYLDTYDIDQ 443
QY 337 MGFPRPVILLENEANQLTDTALQIPAEIGITDVVPAPFRT-----EPINGODA 385
DB 444 PEDGERPI-HEKYTHLCHATAISKSTPPYDNATPIPFMTTHRSAAFYNRIPNKTIKPIA 502
QY 386 IRIWE-----SFTSGPFGFT-----YVDSPOKOKYKIIYRIANNLSAS 423
DB 503 YKMYKLGDTSTVVGKPGFGDLVKGSGNGYIGDIKATVNSPLSQNYRVRVYATNVSGQ 562
QY 424 TVSLTYNN-----QTFPDILNTSLDPNGVAGNGSYTLVE-GPIIEFSQGTNIFKLG-- 475
DB 563 --FNYSNDKITTLQRFQNTVETI--GEGKDLTYGSGFYIEYSTTTPDDKHPKITLHLT 618
QY 476 --SOKGEFAIDSIIFSPV 491
DB 619 DLSNNSSFYVDSIEFIPIV 636

RESULT 9
AAR37214
ID AAR37214 standard; protein; 1138 AA.
XX
AC AAR37214;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 14-SEP-1993 (first entry)
XX
XX B.t. toxin HD867.
XX
XX Coleopteran pests; Bacillus thuringiensis; insecticide; transgenic;
KW plant; pesticide; Colorado potato beetle.
XX
OS Bacillus thuringiensis; strain HD867.
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XX MO9108693-A1.
 XX 13-MAY-1993.
 XX 06-NOV-1992; 92WO-US009510.
 XX 06-NOV-1991; 91US-00788638.
 XX (MYCO) MYCOGEN CORP.
 XX Payne JM, Fu JM;
 XX WPI: 1993-167285/20.
 XX N-PSDB; AA041745.
 XX Control of coleopteran insect pests using bacillus thuringiensis - using
 XX strains Bt HD 511, HD 867 or HD 1011 or their toxins or nucleotide
 XX sequences.
 PS Claim 10; Page 20-22; 29pp; English.
 XX The DNA sequence encoding Bacillus thuringiensis strain HD867 toxin may
 XX be used in an insecticide/pesticide for treatment of Coleopteran pests,
 XX esp. the Colorado potato beetle. Strain HD867 and recombinant cells
 XX contg. the gene encoding the toxin may be treated by chemical or physical
 XX means to prolong the pesticidal activity of the cells, the treated cells
 XX acting as a protective coating for the pesticidal toxin, which becomes
 XX available upon ingestion by a target insect. The compn. may be applied
 XX to the environment of the coleoptera, e.g. plants, soil or water, by
 XX spraying, dusting, etc. See also AAR37214. (Updated on 25-MAR-2003 to
 XX correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
 SQ Sequence 1138 AA;

Query Match 8.6%; Score 220.5; DB 2; Length 1138;
 Best Local Similarity 22.5%; Pred. No. 2,3e-10;
 Matches 124; Conservative 78; Mismatches 213; Indels 137; Gaps 24;

QY 7 TGVITQFRIANDNFRIYAKLFQSTNOSDLYPVLTLPIRAQACVHMLMLKDARTSWG 66
 DB 155 TVIDRFRIIDLAFSSYMPSPFVA-----GYEIPILTVYAQAAMHLALLDST----- 203
 QY 67 QOIDSQNGYKAEILRIKVTNDVNTYNOGLEEKRPKNYGDPEYIOAQRPLDS 125
 DB 204 -----LNGDKWEFTQ-----NNLEENYNR-----QKHISEYSHCVKWNSSG----- 241
 QY 126 VLRNFKVEMKNNKVAKYKGMAMSALEALFPFPGPNYPKQALKVQSRQIFAPVIGI 185
 DB 242 LSRNGSTYEQHINRFRREMLIMWLIDIAVFPIYDPRMSEMTSTQUTREVTYDPLSL 301
 QY 186 PGGITSDSGPTFGSM-RPDVXTYDIDALRQLMELIYQPLKSAVFIYESDMKVRATV 244
 DB 302 -SISNPGIGSPFSQMENTAIRTPHLVDYDEL-----YITSKYKAFSHSI 346
 QY 245 NDIYIGKSGNTGAAMTMS-----SPPSAYIYGAU--CAAGYAPNVVGVRYSHGSGY 294
 DB 347 QPDL-----FYWSAHKVPKOSBOSNLYTTGIVKISGYISS-----GAY 386
 QY 295 T-KGMAPANTNAYAPPEFYKYP---GYKHSVAGYL-----SKAPDAASVWF 338
 DB 387 SRGRNDIYRTLA-ABSUVVYPTTONYGVEFYGKGVHRYGRDNKLDITDSDQLP 445
 QY 339 GRRPVLENEANQLTDTALQIPAEIGITDVVPAFRTE-----EPINGODAIR 387
 DB 446 DEEPI-HEKYTRHLCHATAISKSTPDYDNATIPFESWTRSAEYVNRIVPNKITIPAVK 504
 QY 388 IWE-----SFTSGFGFT-----YVDSPOKOKKIIRIANNISASV 425
 DB 505 MYRLGDTSTVVKPGTGGDLVYKSGNGYIGDIKATVNSPLSONKRVRRVATVNSGQPN 564
 QY 426 SLTVNNQTFPTDILNT-SLDPNGVGNNGSYTLVE-GPIIEFSQGINIFKLG-----SQKG 479

DB 565 VYINDKITLQKRFONTVEITIGEGDLTYGSGFYIEYSTTIQPDKHPKITLHLSLNNNS 624
 QY 480 EFAIDSIIFSPV 491
 DB 625 SFYVDSIEFIPV 636
 RESULT 10
 AA000419
 ID AA000419 standard; protein; 1186 AA.
 AC AA000419;
 DT 11-MAY-2001 (first entry)
 DE Bacillus thuringiensis Cry1Fa/Cry1Ca (FPC1) hybrid insecticidal toxin.
 KW Insecticidal agent; hybrid toxin; FPC1; Cry1Fa; Cry1Ca; insect control;
 KW pest control; crop; insect resistant plant; transgenic plant;
 KW crystal protein; mutant; mutein.
 OS Bacillus thuringiensis.
 OS Synthetic.
 OS Key Location/Qualifiers
 FT Domain 1..445
 FT /note= "Domains I and II from Cry1Fa"
 FT Region 446..454
 FT /note= "Homologous crossover region (junction) between
 FT domain II from Cry1Fa and domain III from Cry1Ca"
 FT Domain 455..1186
 FT /note= "Domain III from Cry1Ca"
 XX WO200114562-A1.
 XX 01-MAR-2001.
 XX 17-AUG-2000; 2000WO-EP008042.
 XX 19-AUG-1999; 99US-00377511.
 XX (SYNG-) SYNGENTA PARTICIPATIONS AG.
 PI De Maagd RA, Borsch HJ, Carozzi NB, Warren GW;
 DR WPI: 2001-218452/22.
 DR N-PSDB; AAS00420.

Novel hybrid insecticidal toxin useful for controlling insects such as
 Spodoptera exigua and Plutella xylostella, comprises domains I and II
 from Cry1F or Cry1B toxin joined to domain III from Cry1C toxin.
 Claim 20; Page 77-81; 99pp; English.

The present sequence represents 1 of 3 novel hybrid insecticidal toxins
 (AA000419-AA000421) and is designated FPC1. FPC1 comprises domains I and
 II from the Cry1Fa toxin at the N-terminus joined to domain III from
 Cry1Ca toxin at the C-terminus. In the 1186 amino acid FPC1 hybrid
 sequence, the junction between the Cry1Fa and Cry1Ca toxin domains
 corresponds to FPC1 residues 446-454. In the 1221 amino acid BHC13 and
 BHC15 hybrid sequences, the junction between the Cry1Ba and Cry1Ca toxin
 domains is residues 482-488 in the BHC13 hybrid, and residues 491-494 in
 the BHC15 hybrid. The hybrid toxins are constructed by cloning and in
 vivo recombination. The hybrid toxins are useful for controlling an
 insect such as Spodoptera exigua (beet armyworm), Manduca sexta (tobacco
 hornworm), Plutella xylostella (diamondback moth), Ostrinia nubilalis
 (European corn borer), Spodoptera frugiperda (fall armyworm), and
 Heliothis virescens (tobacco budworm) which are major causes of
 vegetable, fruit or ornamental flower crop losses. The nucleotide
 sequences encoding the hybrid toxins are useful for producing an insect-
 resistant plant by introducing the nucleotide sequence into the plant
 preferably a transgenic plant. The nucleotide sequences can also be
 expressed in microorganisms such as a virus, bacterium and fungus and the

CC toxin produced used as an insecticidal agent. Baculoviruses engineered
 CC with the nucleotide sequence encoding a hybrid toxin can be used to
 CC infect insects in vivo resulting in their death. The hybrid toxins have a
 CC greater toxicity level than either of their parent toxins alone
 CC
 SQ Sequence 1186 AA;

Query Match 8.4%; Score 214; DB 4; Length 1186;
 Best Local Similarity 21.1%; Pred. No. 9.6e-10;
 Matches 127; Conservative 77; Mismatches 184; Indels 214; Gaps 28;

10 ITQFRIINDNFYIAKLQFSTNOSDQ-----YPL 41
 95 ITTLRLADSYEYIALREWEANPNAQUREDRIRFANTDDALITAINFTLSFEIP 154
 42 TLPLRAQACVMHMLKADATTSVWGQIDSOQLNGYKAEILRLIKYTDVNTVYNOGE 101
 155 LLSVYVQAANLHSLRLDAVSFGQGWGLDIATVNNHYNLINDIHHYTHGCDTVOGGE 214
 102 LEKAKPLNYSDEPEYLOAGRPDISVRSNFKYMKKNKAKYKKGAMASLSLALPPTF 161
 215 -----NLNGITWTRQ---WAFNPOFRDLITLTVLIDIALFPNY 248
 162 G-PNVKQALKVVSROIF-----APY-IGPGGITSQDSGPTFGSMRPDYKTYDQID 212
 249 DVRTPIOTSSQL-TREITTSVIEDSPVSANIPNG-----PNRAEFGVRPPHMD 298
 213 ALRQIMELYIOPLSAIFYESDMKVRATYVNDYIGKGS-----NTGAAMHMSD 265
 299 FNNSLP-VTAETVRS-----QTVMGHLVSSNRTGNRINPFSYGVFPNGAIWADSD 351
 266 PSAITYS-----ALGAAGYAPNVVVR---YSHGSGYTKGM-----APANTN 304
 352 PPPFRTTLDPVFVRGFGNPHYVGLRGVAFOQGTNHTRTFRNSGITDSDDEIPDON 411
 305 AVAPFE-----FKYPGYKLSVSAVGLSKAPDAADSVMPGF--RPVLLNEANQ 351
 412 SGAPMNDYSHVNLHTFVRMPG---EISGSDSWRAP-----WFSMHRSATLTNTID- 460
 352 LITDIALQIPAEIGTIDVVPARFTEEPINGODAIRIM--ESFTSGFGFT----- 399
 461 -----PERINGIPLVKG-----RVMGIGTVITQPGFTGDIARRNF 498
 400 -----YVDSPOKOKYKIYRIANNLASTVSLT----- 428
 499 GDFVSLQVAINSPITQRYRLRFYASRDARVILVGAASGVGQVSVNMPLOKTMETG 558
 429 --YNNQTF-FTDILNTSLDPNGVGNVGYSTLVEGPIIEFSQGTNIFKLG--QXGEFAD 484
 559 ENLTSRTFRYIDFSN---PFSFRANPDIIIGISEOP-----LFGAGSISGGLYTD 605
 485 SI 486
 606 KI 607

RESULT 11
 AARS4073
 ID AARS4073 standard; protein; 1167 AA.
 XX
 AC AARS4073;
 DT 02-FEB-1995 (first entry)
 XX
 DE CRYET4.
 XX
 KW CRYET4; CRYET5; Lepidoptera; lepidopteran insect; insecticidal; toxin;
 XX insecticidal crystal protein; ICP.
 OS Bacillus thuringiensis.
 PN
 XX US5322687-A.

PD 21-JUN-1994.

PF 29-JUL-1993; 93US-00100709.

PR 29-JUL-1993; 93US-00100709.

XX (ECOG-) ECOGEN INC.

PI Tan Y, Jany CS, Donovan WP, Gonzalez JM;

DR WPI: 1994-199503/24.

DR N-PSDB; AA064111.

PT Isolated cryET4 gene and Bacillus thuringiensis cultures transformed with
 this gene - used in compens. against lepidopteran insects.

Claim 1; Col 15-24; 51pp; English.

CC B. thuringiensis strain EG5847 exhibits insecticidal activity against

CC lepidopteran insects. Two novel toxin genes from B. thuringiensis EG5847

CC designated cryET4 and cryET5 produce insecticidal proteins with activity

CC against a broad spectrum of lepidopteran insects. The gene sequences are

CC given in AA064111-12

XX

XX

SQ Sequence 1167 AA;

Query Match 8.2%; Score 210.5; DB 2; Length 1167;
 Best Local Similarity 21.9%; Pred. No. 2e-09;

Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

3 EPPSTGVITQRIINDNFYIAKLQFSTNOSDQYPLTLPPLRAQACVMHMLKADATT 62

123 EAKSRVVIDRRIIDGLIENIPSEFI-----IGFEVPLSVYVQAANLHALLRDSV- 175

63 SVWGQO--IDSOQLNGYKAEILRLIKYTDVNTVYNOGLELEKAKPLNYSDEPEYLOAG 120

176 -IFGERKGLITKRVNDYINRQIREIHEYSNHCVDITYNLE----- 215

121 RPDISVLSNFKPEVMKKNKAKYKKGAMASLSLALPPTFGPN-YPRQALKVVSROIF 179

216 -----RLGFRSIAQWRINYQFRRELTLTVLIDIALFPNDSRLPIQTSQRLREIVT 268

180 APVIGIPGGITSQDSGPTFGSMRPDYKTYDQIDALROL-----NELYIOPLSAIFYW-- 231

269 SPVSEFFYGVYI-NSGNIIGTL-----TEQOIRPRLMDPFNSMIMYTSNDRREHYWGL 321

232 ---IY-----ESDMKVRATYVND-----YIGKR 251

322 EMTAYFTFGAQNVSFLVGRGSAPPLVRSVNDGIYRILSAPFYAPPLGTVLDSR 381

252 GSNTGAAMHMSDPSAITYTSALGAAGYAPNVVGVRSYHSGSYTKGMAPANTNAVAPPEF 311

382 GEKFDPALNNISPPSTIYRH-----PGTVDSLVSI-----PQDNSVFP-- 421

312 KYPGYKLSVSAVGLSKAPDAADSVMPGF--RPVLLNEANQLTDTLQIPAEIGTIDV 369

422 -----HRGSHRSLSHVTMRASSPIFMTIRSATTTNTIN---FNALIQIP-----L 464

370 VPAFRTTEPINGQAIRIWESFTSGFGFT-----YTVSPQOKOKYKI 412

465 VKAFNLH---SGATVVR-----GPGFTGDIIRNTYTGFPADMRVNTIGPLSQRKRV 513

413 IYRIANNLASTVSLTYNNQTFETDILNTSLDPNGVGNVGYSTLVEGPIIE----- 464

514 RIRY-----ASTTLD-----QFFRINTSTVN---QGNF-QRTMNRDNDLESQNFRTAG 558

465 -----FSQGNIFPLGSQ---KGFAIDSLIFSP 490

559 FSTPFSFSAOSTFTLTGTQAFSNOEVYIDRIEFVP 593

RESULT 12
 AAM35258

AAW35258 standard; protein; 1167 AA.
 AAW35258;
 17-FEB-1998 (first entry)
 Bacillus thuringiensis crystal toxin CryET4.
 EG7279; crystal toxin; CryET4; lepidopteran pest; Heliothis virescens;
 Helicoverpa zea; Lymantria dispar; Ostrinia nubilalis;
 Pseudoplusia includens; Plutella xylostella; Spodoptera exigua;
 Spodoptera frugiperda; Trichoplusia ni.
 Bacillus thuringiensis.
 US5679343-A.
 21-OCT-1997.
 07-JUN-1995; 95US-00474038.
 29-JUL-1993; 93US-00100709.
 30-DEC-1993; 93US-00176865.
 (MONS) MONSANTO CO.
 Jany CS, Gonzalez JM, Donovan WP, Tan Y;
 WPI, 1997-525682/48.
 N-PSDB; AAT95050.
 Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to
 control Lepidopteran pests.
 Claim 1; Col 15-24; 50pp; English.
 The present sequence is the Bacillus thuringiensis EG7279 crystal toxin
 CryET4, which, optionally in association with B. thuringiensis EG7279,
 can be used against lepidopteran pests. CryET4 is especially useful for
 controlling Heliothis virescens, Helicoverpa zea, Lymantria dispar,
 Ostrinia nubilalis, Pseudoplusia includens, Plutella xylostella,
 Spodoptera exigua, Spodoptera frugiperda and Trichoplusia ni
 Sequence 1167 AA;
 Query Match 8.2%; Score 210.5; DB 2; Length 1167;
 Best Local Similarity 21.9%; Pred. No. 2e-09;
 Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;
 3 EPPSTGVITQFRILNDNFYKTAQLOFSTNOSDLOYPVLTFLRAQACVHMLMKDATT 62
 123 EAAKSRVLDREFRILDLGLRANIPSPRI-----IGFEVPLLSVYQAANTLALRLDSV- 175
 63 SWNGOO--IDSOQLNGYKAEILRLIKVYNDVNTYNOGLEKAKPLNYSDEEYLQAG 120
 176 -IFGRWGLTTXVNDIYRQIREIHEYSNHCVDYTNLE----- 215
 121 RPDISLRNFKVKNVAVYKKGMAASLSALPPTFGPN-YPKQALKVOSRQIF 179
 216 -----RLGFRSIAQWRIYNOFRRLTLTVDIVALFNVYSRLYPIQTSQLRREIYT 268
 180 AAVYIGITSGDGFPTGSMKRFVKYTDQIDALRQL-----MELYIOPLSAIFW--- 231
 269 SFVSEFYGVV--NSGNIIGTL-----TEQQRRLPLMDPFNSMTMYSDNREHYWSGL 321
 232 ----IY-----ESDMKVRANYVND-----YIGKR 251
 322 EMTAYFTGAGAGVSPVLTGTGSGAPPLTASVNDGIRIISAPYSPALGTVLGSR 381
 252 GSNTGAAMWMSSDPSAIYTSALGAGYAPNVVGVYRSHSGSYTKGMADANTNAYAPPEF 311
 382 GKFPDPAIANNISPPPESTIYRH-----PGTVDSLVS-----PPQNSVVP--- 421

312 KYPGKLVSVAYGLSKAPPAADSVMFGF--RPVLLNEANQLLTOTALQIPAEIGITDV 369
 422 -----HRGSSHLRSHVTRKASSPIFHMTWRSATNTNTIN---PNAIIQIP-----L 464
 370 VPARGTEBPINGODAIRMESFTSGFGFT-----YTUDSPQOKYKI 412
 465 VKARNLH-----SGATVVR-----GPGFTGGDILRRTNTGTADMKEVNTGPIUSORRV 513
 413 IYRLANNLSASTVSLTYNNQTFPTDILNTSLDPNGVRGNYSYTLVEGPITE----- 464
 514 RIRY-----ASTTL-----OFFRINTGSVN---QGNF-QRTMANGDNLESQNFRTAG 558
 465 -----FSQGTNIFKLSQ--KGEFAIDSIIFSP 490
 559 FSTPFSFNAQSTFTLTGTQAFSNOGVYIDRIEFVP 593
 RESULT 13
 AAM17700
 ID AAM17700 standard; protein; 1167 AA.
 AAM17700;
 25-MAR-2003 (revised)
 DT 07-JUL-1997 (first entry)
 CryET4.
 CryET5; CryET4; Bacillus thuringiensis, insecticidal crystal protein;
 ICP; toxin; CryI protein; lepidopteran insect; insecticide.
 Bacillus thuringiensis.
 US5616319-A.
 01-APR-1997.
 30-DEC-1993; 93US-00176865.
 29-JUL-1993; 93US-00100709.
 (MONS) MONSANTO CO.
 Gonzalez JM, Donovan WP, Tan Y, Jany CS;
 WPI, 1997-212077/19.
 N-PSDB; AAT68435.
 Bacillus thuringiensis cryET5 gene encoding insecticidal protein - useful
 for control of lepidopteran pests.
 Example 3; Col 15-24; 50pp; English.
 This sequence represents the cryET4 protein of Bacillus thuringiensis
 (B.t.) isolate EG5847. B.t. produces inclusions during sporulation which
 include insecticidal crystal proteins (ICP). ICP toxins are active in
 insects only after ingestion. Once ingested, the toxic components disrupt
 the midgut cells, resulting in cessation of feeding, and eventually
 death. The CryI proteins produced by B.t. are active against lepidopteran
 insects. This protein, and the CryET5 protein (see AAM17699) belong to
 the CryI family of ICPs. The DNA encoding this sequence can be used to
 transform bacteria, which are useful as insecticides against a wide range
 of lepidopteran pests, and can be applied to crops, soil and seeds. This
 protein, or especially its toxic N terminal region, can be expressed in
 plants, to provide protection against lepidopteran pests. The gene
 encoding this sequence, or its fragments, can also be used to isolate
 other similar genes. (Updated on 25-MAR-2003 to correct PF field.)
 Sequence 1167 AA;
 Query Match 8.2%; Score 210.5; DB 2; Length 1167;
 Best Local Similarity 21.9%; Pred. No. 2e-09;
 Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

```

OY      3  EPPSPGVITQFEIILNDNFILKYLAKQFSTNOSDLOQPVLTLPRLAQACVCHMLMLDQATF 62
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      123  EAKSRVVIDRFRLIGLGLFEANIPSEFI-----IGFEVPLLSYVQANLHLALDSDV- 175
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      63  SVWGQO--IDSCOLNGYKAEILRLIKVYTNVDVNTYTNQGLELEKAPLWNSDEEYLQAG 120
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      176  -IFGRWGLTGNVNDIYNRQIREIHESYNHCDVYNTLE----- 215
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      121  RPDIVLSNFEKWKMKVAKYKQGMASLSLALFPFGCN-YPKQALKVYSGRQIF 179
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      216  -----RIGFSGSIQMRLYNFOFRELTLTVLIDVALFPNYSRLPLPIQTFSSOLTREIYV 268
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      180  APVIGPGGITSQDSGPTFGSMRFDVKYDDOIALRQL-----MELYIQPLKSAFWM--- 231
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      269  SPVSEFFYIGV--NSGNIIGTL-----TEQQRRLPHLMDFNSMIMYTSQNRREHYMSG 321
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      232  --IY-----ESDMKVRAITYND-----YIGKR 251
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      322  EMTAIFFTGAGAQVSPFLVGTGEGSAPPLTVASVNDGIYRLISAPFYSAPELGTIYLSGR 381
           ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      252  GSNTGAAMHMMSSDPSAITYTSALGAAGVAPNVYGVRYSHGSGSYTKGMAPANTNAVAFEE 311
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      382  GEKPFDFALNNISIPSPSTIYRH-----PGTVDSLVS-----PPQDSVSP-- 421
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      312  KYPGVKLSVSYAGSKAPDAADSVWGF--RPVLLLENANQLLDTALQIPAEISITDV 369
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      422  -----HRGSHRISHVTRARASSPFFHHYHSAATTNTITN--PVALIQLP-----L 464
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      370  VPAFGRTTEEPINGODAIRIMESFTSGGFGT-----YTVDSPOKQKYK 412
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      465  VKAFILH-----SGATVVR-----GPGETGGDILKRTNTGTADMRVNI TGPLSQRYV 513
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      413  IYRIANNLSASTVSLTYNNQTFPTDLNLSLDPNGVGRGVGSGTYLVEGPPIE----- 464
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      514  RIRY-----ASTTDL-----QEFFRLNGTSVN-----QGNF-QRTNMRGDNLESGNERTAG 558
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      465  -----FSQGTNIFKLGSQ--KGEFAIDISIFSP 490
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      559  FSTPFSFSMAOSTFTLGTQAFNSQEVYIDRIEIVP 593
           |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 14
AAM87632
ID      AAM87632 standard; protein; 1167 AA.
AC      AAM87632;
AD      03-MAR-1999 (first entry)
DE      CRYET4 protein sequence.
KW      CRYET4; Bacillus thuringiensis strain EG5847; crystal toxin; CRYET5;
        Lepidoptera; Helicoverpa zea; resistant strain; Plutella xylostella;
        Spodoptera exigua; S. frugiperda; S. frugiperda; Trichoplusia ni.
OS      Bacillus thuringiensis.
PN      US5854053-A.
PD      29-DEC-1998.
PE      06-JAN-1997; 97US-00779046.
PF      29-JUL-1993; 93US-00100709.
PR      30-DEC-1993; 93US-00176865.
PR      07-JUN-1995; 95US-00474038.
PA      (ECOG-) ECOGEN INC.
PI      Donovan WP, Gonzalez JM;
PP      WPI; 1999-094915/08.

```

Query Match	8.2%; Score 210.5; DB 2; Length 1167;	
Best Local Similarity	21.9%; Pred. No. 2e-09;	
Matches 126;	Conservative 70; Mismatches 188; Indels 191; Gaps 26	
3	EPSPSGVITQRIILNDNFIKYAKIQFSTNSDLDYPIITLPLRQACMHLMLKDAT	62
123	EAKSRVVIDRPFILDLGLIEANIPSFRI-----IGFEVPLLSVYQVANLIALRLDSV-	175
63	SVWGQO--IDSQQLNGYAKAELIRLIKVTYNDVNTYNOGLELEKAKPLNYSDEEYLQAG	120
176	-IFGRMKGLITKNVVDIYNQRIREIHEHSNHCVDYTNELH-----	215
121	RPDISVLRSNFEVKNKVKAKYKGMMSALSLALPFTFGPN-YPKQALKVOSRQIF	179
216	-----RLGFRSIQMRIRYVQFRELTLTVLIDIVALFPNYSRLYPIQTFSQLTREIVT	268
180	APVIGIPGGITISQDSGPTFGSKRFPVKYKYDOIDALRQL-----MELXIPLKSAIYVW-	231
269	SPVSEFFYYGYI--NSGNIIGTV-----TEQQRIRPHLMDFFNSMTMYTSDNRREHYWGL	321
232	--IY-----ESDMKVRATYVND-----YIGKR	251
322	EMTAYFTFGAGAOVSFPLVGRGESAPELLYTRASVNDGIRILASAFYSAPFLGTYLGSR	381
252	GSNTGAAMHMMSSDSAIYTSALGAAGYAPNVGVGRYSHGGSYTKGMAPANTNAYAPFEF	311
382	GEKEDFALNNISPPSTIYRH---PGTVDSLVS-----PQDNSVDP-----	421
312	KTPGYKLHSVSAVYGLSKAPDAADSVMGFP--RPVLEANEANOLLDTALQIPAEIGITDV	369
422	-----HRGSGHRSLSHTYTRMASSPIFFMWTHTRSATTTVTIN---FNALIQID-----L	464
370	VPAFRTETEPINQDAIRIWESFTSGFGPT-----YTVDSPOKOKYKI	412
465	VKAEFLH---SGATVVR-----GPGTGGDILIRKNTGTGADMRVNIITGPPLSORYRV	513
413	IYRIANLNSASTVSLTYNNOTFFETDILNTSLDPNGVRGNVGSYTLVEGPIIE-----	464
514	RIRY-----ASTLD-----QFFIRINGTSVA-----QGNF-QRTNMRGNLSEGNFRTAG	558
465	-----FSQGTNIFKLGSQ---KGEFAIDSIIFSP	490
559	FSTPFSFSMAQSTFLTGQAFNSQGVYIDRIEFVP	593

Sequence 1167 AA;

Query Match 8.2%; Score 210.5; DB 2; Length 1167;
 Best Local Similarity 21.9%; Pred. No. 2e-09;
 Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26

3 EPPSGVITQRIILNDNFIKYAKIQFSTNSDLDYPIITLPLRQACMHLMLKDAT 62
 123 EAKSRVVIDRPFILDLGLIEANIPSFRI-----IGFEVPLLSVYQVANLIALRLDSV- 175
 63 SVWGQO--IDSQQLNGYAKAELIRLIKVTYNDVNTYNOGLELEKAKPLNYSDEEYLQAG 120
 176 -IFGRMKGLITKNVVDIYNQRIREIHEHSNHCVDYTNELH----- 215
 121 RPDISVLRSNFEVKNKVKAKYKGMMSALSLALPFTFGPN-YPKQALKVOSRQIF 179
 216 -----RLGFRSIQMRIRYVQFRELTLTVLIDIVALFPNYSRLYPIQTFSQLTREIVT 268
 180 APVIGIPGGITISQDSGPTFGSKRFPVKYKYDOIDALRQL-----MELXIPLKSAIYVW- 231
 269 SPVSEFFYYGYI--NSGNIIGTV-----TEQQRIRPHLMDFFNSMTMYTSDNRREHYWGL 321
 232 --IY-----ESDMKVRATYVND-----YIGKR 251
 322 EMTAYFTFGAGAOVSFPLVGRGESAPELLYTRASVNDGIRILASAFYSAPFLGTYLGSR 381
 252 GSNTGAAMHMMSSDSAIYTSALGAAGYAPNVGVGRYSHGGSYTKGMAPANTNAYAPFEF 311
 382 GEKEDFALNNISPPSTIYRH---PGTVDSLVS-----PQDNSVDP----- 421
 312 KTPGYKLHSVSAVYGLSKAPDAADSVMGFP--RPVLEANEANOLLDTALQIPAEIGITDV 369
 422 -----HRGSGHRSLSHTYTRMASSPIFFMWTHTRSATTTVTIN---FNALIQID-----L 464
 370 VPAFRTETEPINQDAIRIWESFTSGFGPT-----YTVDSPOKOKYKI 412
 465 VKAEFLH---SGATVVR-----GPGTGGDILIRKNTGTGADMRVNIITGPPLSORYRV 513
 413 IYRIANLNSASTVSLTYNNOTFFETDILNTSLDPNGVRGNVGSYTLVEGPIIE----- 464
 514 RIRY-----ASTLD-----QFFIRINGTSVA-----QGNF-QRTNMRGNLSEGNFRTAG 558
 465 -----FSQGTNIFKLGSQ---KGEFAIDSIIFSP 490
 559 FSTPFSFSMAQSTFLTGQAFNSQGVYIDRIEFVP 593

RESULT 15
 AAY30922
 AAY30922 standard; protein, 1167 AA.
 AAY30922;
 18-OCT-1999 (first entry)
 B. thuringiensis cryET4 protein.

XX Toxin; cryET4; cryET5; insecticidal; lepidoptera; transformed plant;
 KW crystal protein; insect.
 XX
 XX Bacillus thuringiensis.
 XX
 XX US5942658-A.
 XX
 XX 24-AUG-1999.
 PD
 XX
 XX 24-JUN-1997; 97US-00881340.
 XX
 XX 29-JUN-1993; 93US-00100709.
 PR 30-DEC-1993; 93US-00176865.
 PR 07-JUN-1995; 95US-00474038.
 XX
 XX (MONS) MONSANTO CO.
 XX
 XX Gonzalez JM, Jany CS, Tan Y, Donovan WP;
 PI
 XX WPI; 1999-493544/41.
 DR N-PSDB; AA209159.
 DR
 XX
 XX Transformed plant comprising insecticidal crystal proteins.
 PT
 XX
 XX Claim 1; Fig 1A-J; 50pp; English.
 PS
 XX
 XX This invention describes novel transformed plants containing Bacillus
 CC thuringiensis strain EGS847 insecticidal crystal protein genes cryET4 or
 CC cryET5. cryET4 and cryET5 are novel toxin genes which produce
 CC insecticidal proteins with activity against a broad spectrum of insects
 CC of the order Lepidoptera. This represents the cryET4 protein described in
 CC the method of the invention

SQ Sequence 1167 AA;

Query Match 8.2%; Score 210.5; DB 2; Length 1167;

Best Local Similarity 21.9%; Pred. No. 2e-09; Matches 126; Conservative 70; Mismatches 188; Indels 191; Gaps 26;

QY 3 EPPSTGVITQPIILNDNFIKYLAKQFSTNQSGLQVPVLTPLRAQACVMEHMLKDAVT 62
 DB 123 EAKRSRVIDRFRILDGLIEANIPSPRI-----IGFEVPLSVYQANLHIALRDSV- 175
 QY 63 SVMGQO--IDSOQLNGYKAEILRLIKVYTNVNTYNOGLEKAKPLNYSDBEYLQAG 120
 DB 176 -IFGRMGILTGNVNDIYNRQIREIHEYSNHCVDTYNTELE----- 215
 QY 121 RPDISVLNSNFEKVKMKNVAKYKGMMSALSIALPFTFGPN-YPKQALKVYQSRQIF 179
 DB 216 -----RLGFRSLAQWRIYNQFRRELTLTVLIDVALFPNYSRLYPIQFSQLTREIYT 268
 QY 180 APVIGIPGGITSDSGPFGSMRPVKYTDQIDALROL-----MELYIOPLKAYFW-- 231
 DB 269 SIVSEFYGVLT--NSGNITGLT-----TEQIRRHLMDFRSMIMYTSNDRREHYMSG 321
 QY 232 ---LY-----ESDWKVRATYVND-----YIGKR 251
 DB 322 EMTAYFTGPAQAQVSPPLVGTREGESAPPLTVRSVNDGIYRILSAPFYSAPFLGTIVLSGR 381
 QY 252 GSNTGAAMHMSDDPSAITYTSALGAAGYAPNVYGVARYSHGSGYTKGMAPANTNAYAPFEF 311
 DB 362 GKKFDFALNNTISPPSTIYRH---PGTVDSLVS-----PPQDNVSP--- 421
 QY 312 KYPGYKLSVSAVGLSKAPDADSVWFGF--RPVLIENEANQLTDTALQIPAEIGITDV 369
 DB 422 -----HRGSSHRISHVTMRASPIFHTHRSATTNTIN--PNAIIQIP-----L 464
 QY 370 VPAFGRTPEEPINGQDAIRIMESFTSGFGFT-----YTVDSPQOKYKI 412
 DB 465 VKAFNLH---SGATFVR-----GPGFTGDDILARTNTGTFADMRVNTGTPLSQRYRV 513
 QY 413 IYRIANNLSASTVSLTYNNQTFFTDILNLSLDPNGVGNVGSYTLVEGPILIE----- 464

DB 514 RIRY-----ASTDL-----QFFTRINGTSYVN-----QGNF-QRTMNRGDNLESQNFRTAG 558
 QY 465 -----FSQGTNIRKLSQ---KGEFALDSIIFSP 490
 DB 559 FSTPFSFSMAOSTFTLTGTQAFSNQEVYIDRIEFVP 593

Search completed: October 19, 2005, 20:14:37
 Job time : 169 secs

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OM protein - protein search, using sw model

Run on: October 19, 2005, 20:08:06 ; Search time 42 Seconds
(without alignments)
1127.111 Million cell updates/sec

Title: US-10-756-778-8
Perfect score: 2560
Sequence: 1 IAEPPSTVITQFRIINDNF.....KLSGSKGFALDSIFSPV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR 79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228.5	8.9	1138	2 A48944	parasporal crystal
2	207.5	8.1	1174	2 S32649	parasporal crystal
3	200	7.8	1174	2 A42459	parasporal crystal
4	199.5	7.8	1156	2 A29838	parasporal crystal
5	196	7.7	1157	1 S49247	parasporal crystal
6	194	7.6	659	2 S10228	parasporal crystal
7	186	7.3	1155	2 A26513	parasporal crystal
8	186	7.3	1155	2 JDU0002	parasporal crystal
9	186	7.3	1156	2 A29125	parasporal crystal
10	184.5	7.2	1181	2 A41052	parasporal crystal
11	184	7.2	649	1 JH0261	parasporal crystal
12	184	7.2	1155	2 S02134	parasporal crystal
13	184	7.2	1155	2 I39838	parasporal crystal
14	183.5	7.2	1289	2 T18212	parasporal crystal
15	183	7.1	1385	2 T18213	parasporal crystal
16	181.5	7.1	719	2 I40590	parasporal crystal
17	177	6.9	1154	2 S39536	parasporal crystal
18	177	6.9	1160	2 S32647	parasporal crystal
19	176	6.9	1228	2 S00873	parasporal crystal
20	174	6.8	652	2 I39811	parasporal crystal
21	174	6.8	652	2 A27323	parasporal crystal
22	174	6.8	1189	2 S00944	parasporal crystal
23	172.5	6.7	1176	2 A48970	parasporal crystal
24	172	6.7	655	2 JCT140	parasporal crystal
25	169.5	6.6	719	2 I39814	parasporal crystal
26	169.5	6.6	719	2 S25383	parasporal crystal
27	169.5	6.6	1245	2 T18211	parasporal crystal
28	169	6.6	823	2 S04181	parasporal crystal
29	168.5	6.6	719	2 I39815	parasporal crystal

30	168	6.6	1136	1 USBS81	parasporal crystal
31	167.5	6.5	934	2 A22798	parasporal crystal
32	165.5	6.5	1176	2 A22617	parasporal crystal
33	165.5	6.5	1176	2 JCT219	parasporal crystal
34	165.5	6.5	1176	2 JCT021	parasporal crystal
35	165.5	6.5	1176	2 S02215	parasporal crystal
36	162	6.3	1165	2 S11446	parasporal crystal
37	160.5	6.3	934	2 B29838	parasporal crystal
38	159.5	6.2	1160	2 I40589	parasporal crystal
39	156	6.1	1177	2 A49785	parasporal crystal
40	154	6.0	618	2 S11445	parasporal crystal
41	153.5	6.0	633	2 D32053	parasporal crystal
42	151	5.9	633	2 C32053	parasporal crystal
43	151	5.9	1180	2 I39870	parasporal crystal
44	150.5	5.9	1178	1 USBSXH	parasporal crystal
45	148	5.8	1180	2 A26858	parasporal crystal

ALIGNMENTS

RESULT 1	A48944	parasporal crystal protein cry7Aa1 - Bacillus thuringiensis
N:Alternate names:	parasporal crystal protein cryIIIC	
C:Species:	Bacillus thuringiensis	
C:Date:	19-Dec-1993	#sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession:	A48944	
R:Lambert, B.; Hottel, H.; Anny, K.; Jansens, S.; Soetaert, P.; Peferoen, M.		
Appl. Environ. Microbiol.	58, 2536-2542, 1992	
A:Title:	Novel Bacillus thuringiensis insecticidal crystal protein with a silent activit	
A:Reference number:	A48944; MUID:92384571; PMID:1514800	
A:Contents:	BT8137U	
A:Accession:	A48944	
A:Status:	Preliminary	
A:Molecule type:	DNA; protein	
A:Residues:	1-1138 <LM>	
A:Cross-references:	UNIPROT:O03749; GB:M64478; NID:9142760; PIDN:AAA22351.1; PID:9142761	
A>Note:	Sequence extracted from NCBI backbone (NCBIN:112092, NCBI:P.112093)	
C:Superfamily:	parasporal crystal protein	
C:Keywords:	delta-endotoxin	
Query Match	8.9%; Score 228.5; DB 2; Length 1138;	
Best Local Similarity	22.4%; Pred. No. 9.8e-09;	
Matches	124; Conservative 70; Mismatches 216; Indels 143; Gaps 23;	
QY	9 VITQRIINDNFIRIKYIAKIQSTNQSDIQ-YVLTLPPIRAQACVHMLMDAT--SVW 65	
DB	157 VATEFRIDSLP-----EFSSMPSFKVTGYEIRPLTVYAQAAMHLALDLSDSTLYGDKW 209	
QY	66 G--QQIDSQINGKAEILIRLIKVTNDVNTVNOGLELEKAKPLNYSDBPEYLOAGRPD 123	
DB	210 GFTQNNIENNROK---KRISEYSDHCTKMYNSGLS----- 243	
QY	124 ISVLSNFKKWKNNKVKYKRGMMASLSIALPPTGPNVPKQALKVOSRQIFAVI 183	
DB	244 ----RLNGSTYEQMNTNVRFRREMILMDLVAVPPHDPKRYSMETSTQLTRVYTPV 299	
QY	184 GIPGQITSDGSPPTGSGN-REDVKTYYDQIDALRQIMELYIOLPKSAYWIIYESDMKVRAT 242	
DB	300 SL--SISNPDIGSPSQMENTAIRPHLDVYIDEL-----YIYTSKYKARSH 344	
QY	243 YVNDYIGKSGNTGAAMTMS-----SDPSALYTSAL--GAAGVAPNVGVYSHGG 292	
DB	345 EIQDPL-----FYWSAHKVSFKKSSQSNLYTIGIKTSGYISS--GAYSFGN 391	
QY	293 SYTKGMAPANTNVAAPFEFKYP--GYKLHSAVAYG-----SKAPDAADSVW 337	
DB	392 DIYRTLA-----APSVVVPYTONYGVEQVEFGVGVHVRGDKNYKDYLDYSIDQLP 444	
QY	338 FGFRPVLLNEANQLTTTALQIPAEIGITDVVPAFGTE-----EPINGQDAI 386	
DB	445 PDGEP1-HEKVTYHRLCHATAIFKSTPDYDNATIPFISWTHRSABEYNNIYPNKIKTIPAV 503	

```

OY 387 RIVE-----STSGEGT-----YVDSQKQKYKIYIANLSAST 424
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 504 KMYLDLDBSTVYVKPGFTGGDLVKRGSGTGYIGDKAIYVNSLSOKYRVRVYANVSGOF 563
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 425 VSLTYNNQTFETDILNT-SLDPNGVRNGYSYTLVE-GRPIEFSQTNIFKQ-----SOK 478
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 564 NVYINDKTLTKFQNTVETIGEGKDLTYGSGFYIEYSTTITQFPDEHPKTLHLSDLSNN 623
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 479 GEFAIDSTIEFPV 491
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 624 SSFYVDSIEFIPV 636

RESULT 2
S32649
paraportal crystal protein cry1Fa3 - Bacillus thuringiensis
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S32649
submitted to the EMBL Data Library, April 1993
A:Reference number: S32645
A:Accession: S32649
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1174 <LIM>
A:Cross-references: UNIPROT:Q45749; EMBL:Z22512; NID:g295865; PIDN:CAA60235.1; PID:g29586
C:Superfamily: paraportal crystal protein
C:Keywords: delta-endotoxin

Query Match      8.1%; Score 207.5; DB 2; Length 1174;
Best Local Similarity 22.7%; Pred. No. 3,9e-07;
Matches 131; Conservative 77; Mismatches 200; Indels 169; Gaps 30;

OY 10 ITGRIINDNFIKYIAKI-QFTNSQSDIQ-----YPLV 41
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 95 ITTIRGLADSEVYVLEALREWEENENNNALREDVRIREPANTD DALITAINNFTLTSEIP 154
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 42 TLPLRAQCSWHIMLTKDATTSSVWGQIDSQDLGKYKELRLTKVYNDVNTYNGGLE 101
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 155 LLSVYVQANLHLSLLRDAVSFGQGWGDIATVNNHNRLNLHRYTEHCLDTYNGGLE 214
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 102 LEKAKPLNYSDEEYTLQARPDISVLSNFKEXKWKNNVAKYKRGMMASLSIALPTF 161
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 215 -----NLRGNTNQ-----WSEFNGFRRELTLTVLDIYALPEPY 248
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 162 GPN-YPKALKVVSROIF-----APV-IGIPGCTISQDSGPTFGSMRPDYKTYDQID 212
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 DARAYPIQTSQQL-TREIYTSVIEDSPVSANIPNG-----FNAAEFGVAPPHLMD 298
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 213 ALRQIMELYIQPLKSAYFW--IYESDMKVRATVYNDYIGKRGSMYTGAMMHMSSDPAIY 270
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 FMSNLSF-VTATVTSQTYWGHLVSSRNTAGNPINFIPLYIGNPGALW-IADSDPRPFY 356
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 271 TS-----ALGAAGYAPNVGVVR--YSHGSGYTKGM-----APANTNAYAPF 309
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 RTLSDPVFRVGRFGNPHVVLGLRGVAFPQGTQTNHRTFRNSGCTISDSEITPPQNSGAPW 416
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 310 E-----FKYEGYKLSVSAYGLSKAPDAADSVMGCFRPVLLNEANQLITDTAL 358
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 NDYSHVNLNHTVFRWPG---EIASGDSMRAP-----MFSWTH-RSADRFTNIINPNIT 465
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 359 QIPA-----BIGITDV-VPAFRTEEPINQDARIWESTSGRG-FTTYVDSPOKQY 410
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 466 QIPAVKANHLHSGSTVVRGPGF-----TGQDLRL-RITNGTFADIRVNTGSLSORY 516
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 411 KIIRIANNLASTVSLTYNNQTFETDILNTSLDPNGVRNGYSYTLVEGP1IE-----464
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 517 RVRIRY-----ASTTDL-----QFFTRINGISVN-----QGNF-QRTNMRGANLSSGNPRT 561
      : : : : : : : : : : : : : : : : : : : : : : : :
OY 465 -----FSGQTNIFKLGSGQ---KGFAIDSIIFSP 490
      : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 562 AGSTPFSFSAQSTFTLGTQAFSNOEVDYIDRIEFVP 598

RESULT 3

A42459

paraoporal crystal protein cry1Fa1 - *Bacillus thuringiensis* (strain aizawai)

N:Alternate names: paraoporal crystal protein cry1f

C:Species: *Bacillus thuringiensis*

C:Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004

C:Accession: A42459

R:Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C. J. *Bacteriol.* 173, 3966-3976, 1991

A:Title: Isolation and characterization of a novel insecticidal crystal protein gene from *B. thuringiensis*

A:Reference number: A42459; MUID:91286178; PMID:2061280

A:Accession: A42459

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1174 <CHA>

A:Cross-references: UNIPROT:Q03746; GB:M63897; NID:g142757; PIDN:AAA22348.1; PID:g142758

C:Superfamily: paraoporal crystal protein

C:Keywords: delta-endotoxin

Query Match 7.8%; Score 200; DB 2; Length 1174;

Best Local Similarity 22.0%; Pred. No. 1.4e-06;

Matches 127; Conservative 79; Mismatches 204; Indels 168; Gaps 29;

10 ITGFRILNDFIKYIAKL-QFTNQSDLQ-----YPLV 41

Db 95 ITTLRGADSYEYIEALREWEANPNNAQREDVRIRFANTDDALITAINFTLTSFEIP 154

Qy 42 TLPIRAQACVHMLLKDATTSVWGQIDISQLANGKAEILRLKYTNDVNTYNOGLE 101

Db 155 LLASYVAANLHLISLMDAVSFGQGWGLDIATYNNHNRLINLIHRTKXCLDTYNOGLE 214

Qy 102 LEKAKPLNTYSDPEBYQAGRPRDISVLRNFKFEVKKNNKYVYKRGAMASLSALFPTF 161

Db 215 -----NARGTNRQ-----MARFNGPRDLTLTYLDVALFPRY 248

Qy 162 G-PNYPKQALKVQSRQIF-----APV-IGIPGIGTTSQSGPTGSMKRFVYKYVDQID 212

Db 249 DVRTYPIQTSSQL-TREIYTSVLEDSPVASINPNC-----FNRAEFGVRPHLMD 298

Qy 213 ALRQIMELYIQPLKSAFWMYESDMKRAYVNDYIGKRS-----NTGAAMHMKSSD 265

Db 299 FMSNLF-VTAETVRS-----QYWGGHVSSRNTGAGRINFPSSYGVFNGALIMADED 351

Qy 266 PSALYTS-----ALGAAGYAPNVGV-----YSHGSSYTKGM-----APANTN 304

Db 352 PRPYRTLPDPVFRFGSGFNPHYVLGLRGVAPQOTGTNNHRTTRNSGTIDSLDEIRPODN 411

Qy 305 AYAPFE-----FKYPGYKLHSVSAVYGLSKAPDAADSVMFGRPYLLENANQLL 353

Db 412 SGARWMDYSHVNLHVTFRWPG-----EISGSDSWRAP-----MFGWTH-RSATPNTIID 460

Qy 354 TDRLAQIP-----AEIGITDV-VPAFGRTPEEPINGODAIRIESFTSGGFFITYV--- 402

Db 461 PERITQIPLVKAHTLQSGITVVRGPGF-----TGDDILR-----RTSGGPFYTIWIN 509

Qy 403 -DSQKQKVKIIVRIANLNLASVYSLTYNNQFTFDILNLSLDPNGVRGNGYGS----- 455

Db 510 GQLPQRRAIRARIVASTNL--RIYTVAGERIFACQFNNKMD-TDPLTFQSFSAATTN 565

Qy 456 TLVEGPITE--FSQGTNIFKLGSQKGFADISITFSPV 491

Db 566 TATFPFMSQSSFTYGAADTFSSGN---EVIYIDREELIPV 600

RESULT 4

A29838

paraoporal crystal protein - *Bacillus thuringiensis* subsp. *kurstaki*

C:Species: *Bacillus thuringiensis* subsp. *kurstaki*

C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004

C:Accession: A29838

R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zounes, M.; Wild, M.; Wallfield, A.M.
 J. Bacteriol. 166, 801-811, 1986
 A:Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal
 A:Reference number: A84672; MUID:86223796; PMID:3011746
 A:Accession: A29838
 A:Molecule type: DNA
 A:Residues: 1-1156 <THO>
 A:Cross-references: UNIPROT:P06578; GB:M12661; NID:G143226; PIDN:AAA22613.1; PID:G143227
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 7.8%; Score 199.5; DB 2; Length 1156;
 Best Local Similarity 21.2%; Pred. No. 1.5e-06;
 Matches 128; Conservative 84; Mismatches 174; Indels 217; Gaps 32;

```

QY 8 GVITPRLINDNFITKIA-----KIOFTNSQDL-----QYVUTLPLR 46
DB 102 GLSNLYQIYAESFRWEMADPTNPALREWRIOFDMNSALTTAIPLFAVONYQVPLLSVY 161
QY 47 AQACVHMLMLKDATTSVWGO--IDSOQLNGYKAEIRLIKVTNDVNTYNOGLEEK 104
DB 162 VOANMLHSVLRD--VSFQGRWGFDAATINSRYNDLTRIGNYTDHRYRMTGLE-- 216
QY 105 AKPLNYSPEEYLQAGRDPDISVLRSNFKVEMKMNKAVAKKGMASALSLAALPPTF-GP 163
DB 217 -----RWGPD-----SRDWIRYNGFRRELTLVLVDIYSLFPNYSR 253
QY 164 NYPKQALKVVSQRIIPA-PVI-----GIPGGITSDSGPTGSMRFDVKTYYDQ 210
DB 254 TPIPIVSGQL-TREIYTPVLENFDFGSPFGSAQGIIEGIRSP-----HL 296
QY 211 IDALFQMLIELYIQPLKSAVFIYESDMKVRATYVNDYIGKSGNSGAAH--WMSDPSA 268
DB 297 MDLINSI-TIYDAHREGIYV--SGHQIMASPV---GFSGPETTFPLVGTMGAAAPQ 348
QY 269 IYTSALGAGY-----APNVGVVYSH---CG-----SYTK----- 296
DB 349 RIVAGLGGVTRTSLTYLRPFNGINNOQLSGDGRICLMLNKKGQPYTEKAPV 408
QY 297 ---GMAAPANN-----AVAPFEFKYPGYKLSHVSAYGLSKAPDAADSVMFGRPP 342
DB 409 DSPDEIPQNNNVPRQGFSHRCLAVVSWFSGFNSSVS---VIRAPV-DS----- 456
QY 343 VILEENAOQLDTYLAQIPAEIGITDVVAPRGTEEPINGDAIIMESFTSGPFT--- 399
DB 457 -----SWTYSAEFG--DVLPSSQITQIPITKIQS-WLMNSVWGLGPTGAD 500
QY 400 -----YTVDSPOKOKYKIIYIANNLSASTVSLTYNNQTFPTDILNTSLDPN 446
DB 501 ILEELTGQISTIRVNITAPLSQRYRIRY-----ASTNNLOP-----HTSIDR 545
QY 447 GV-RGNYSGYTLVEGPILR-----FSQGTNIFKLQ---SQKGEPAIDSI 487
DB 546 PINQNF-SATWSSGSNLQSGSFRTVGTTPNFNSGSSVFTLSAHVFNSGEYIDRIE 604
QY 488 FSP 490
DB 605 FVP 607

```

RESULT 5

S49247
 parasporal crystal protein cry9Ca1 (validated) - *Bacillus thuringiensis*
 N:Alternate names: parasporal crystal protein cry1H
 C:Species: *Bacillus thuringiensis*
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #ext_change 09-Jul-2004
 C:Accession: A59350; S49247
 R:Hamberg, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V.
 Appl. Environ. Microbiol. 62, 80-86, 1996
 A:Title: A *Bacillus thuringiensis* insecticidal crystal protein with a high activity aga
 A:Reference number: A59350; MUID:96141404; PMID:8572715
 A:Accession: A59350
 A:Molecule type: DNA

A:Residues: 1-1157 <LAM>
 A:Cross-references: UNIPROT:Q45733; EMBL:Z37522; NID:G547554; PIDN:CA85764.1; PID:G5475
 A:Experimental source: serovar colworthi
 C:Comment: This parasporal crystal protein, active against corn borer and other insects,
 C:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 7.7%; Score 196; DB 1; Length 1157;
 Best Local Similarity 22.3%; Pred. No. 2.8e-06;
 Matches 128; Conservative 77; Mismatches 192; Indels 178; Gaps 28;

```

QY 9 VITPRLINDNFITKIAKLOFTNSQDLQYVUTLPLRAQACVHMLMLKDATTSVWGO 68
DB 169 VRAQFIALDIDFVAIP--LFAVNGQ--QYVPLLS--VYAQVNHLLMLKASLPGEWG 222
QY 69 IDSOQLNGYKAEIRLIKVTNDVNTYNOGLEEKAPLAYSPEEYLQAGRDPDISVLR 128
DB 223 FTQGEISTYDROLELAKRYNTYCEWTNGLDR-----LR 258
QY 129 SNFKVEMKMNKAVAKKGMASALSLAALPPTF-----GNYPKQALKVVSQRIIPAP 181
DB 259 GTNTE--SWLRHQFRREMTLVLDVALFFYDVRLYPTGSN--POLREYVTPPIVENP 315
QY 182 VIGI-----PGITSDSGPTGSMRFDVKTYYDQIDALRQLM 218
DB 316 PANVGLCRMGNTPNYTFSELENAFIRPHLFDRLNSITISNRPV----- 362
QY 219 ELIYIQPLKSAVFIYESDMKVRATYVNDYIGKRS-----NTGAAMHMSDPSAIYTA 273
DB 363 -----SSNFMWYSQHTLRYSYLNDSAVQEDSYGLITTTTRATNGVDGTRIESTA 414
QY 274 LGAGVAPNVVYVR--YSHGGSYTKGMAPAN-----TNAYAPFEFKYPGYKLSHVS 322
DB 415 VDFRSALIGITGVNRASVPGELFRNGTISPAANGCRDLYDNDLPPD-ESTGSSTRLS 473
QY 323 -----AVGLSKAPDAADSVMFGRPVLL---ENEANQLDTYLA-QIPAEIGITDVVA 372
DB 474 HTVFPSPQTNGAGSIANA--GSVPTYVWTRDVLNNTIRPNRITQLP----- 519
QY 373 FGRTEEPINGDAIRIMESFTSG-----FG-FITYVDSPOKOKYKIIYRIAN--N 419
DB 520 LVKASAPVSGTIVK-GPGFVGGLRRTTNGTGTGLRVYNSPLTOQYRLRVRFASGN 578
QY 420 LS-----ASTVS-----LYNNQTFPTDILNTSLDPNGVNGVSGSYTLVEG 460
DB 579 FSIKVLKGVISIGVRLGSLTNMKGELTY--ESFTRPFTTT-----GPF---N 622
QY 461 PIIEFSQGTNIFKLQ---SQKGEPAIDSIIFSPV 491
DB 623 PPIFTTQAGELITVNAEGVSGEYIDRIEIVPV 657

```

RESULT 6

S10228
 parasporal crystal protein cry3Ba1 - *Bacillus thuringiensis* (fragment)
 N:Alternate names: coleopterian-active parasporal crystal protein; delta-endotoxin
 C:Species: *Bacillus thuringiensis*
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #ext_change 09-Jul-2004
 C:Accession: S10228
 R:Sick, A.; Gaertner, F.; Wong, A.
 Nucleic Acids Res. 18, 1305, 1990
 A:Title: Nucleotide sequence of a coleopterian-active toxin gene from a new isolate of *Ba*
 A:Reference number: S10228; MUID:90206811; PMID:2320431
 A:Accession: S10228
 A:Status: translation not shown.
 A:Molecule type: DNA
 A:Residues: 1-659 <STC>
 A:Cross-references: UNIPROT:P17969; EMBL:X17123; NID:G40258; PIDN:CAA34983.1; PID:G40259
 C:Genetics:
 A:Gene: cryIIIB
 A:Superfamily: parasporal crystal protein
 C:Keywords: delta-endotoxin; toxin

[illegible]

Db 102 GLSLNLYQIVAESPFREMEADPTNPALREEMRIQFNDMNSALTTPLPLFAVONYVPLLSVY 161

Qy 47 AQACVHMLMLKQATTTVMGQ--IDSQOLNGYKAEILRIKYVDVNTVNTYNGELEK 104

Db 162 VQANMLHSLVRD--VSVFGQRMGFDAATINSRNDLTRILGNVTHDAVAMNTGLE--- 216

Qy 105 AKPLNSDPEEYLOAGRPDISVLSRNFKEVMKNNKAKYKRGAMSLSLAALPPTF-GP 163

Db 217 -----RWGPD-----SRDWRYNQFRRELTLTYLDIVSLFPNYSR 253

Qy 164 NYPRQALKVQSRIFA-PVY-----GPGGITSQDSGPFPSGRDVKTYDQ 210

Db 254 TYPLRTVSQL-TREIYTNPVLENPDGSLRALQGISGSLSP-----HL 236

Qy 211 IDALRQMLETYIOPLKSAFYIYESDMKVRATYVNDYIGRGSNTGAAMH--MMSDPSPA 268

Db 297 MDILNSTI-TIYTDHREIYVW---SGHQMASPV---GSGGPEFTFPYLYGTMGNAAPQ 348

Qy 269 IYTSALCAAGY-----APNVGV-----RYSHGGS-----YTKG--- 297

Db 349 RIVAQLOGGVYRTLSLTLYRRPFNIGINNQLSVLDGTEFAVGSNLPAAVYRKSGTVD 408

Qy 298 ----MAPNNNAVAPPEFFK-----PGYLHSVSAAGLSKAPPAASVWNGPRPV 344

Db 409 SLDEIPQNNNVPPRGFSHRLSHVSMFSGFSNSVS---ITRAP-----MFSW--- 455

Qy 345 LENEAQQLTDTALQIPAEIGITDVVAPAFRTEEPINGQDAIRIMESFTSGFPT----- 399

Db 456 -----IHRSAEPNNIITPSQITQIPLTRKSNLDSGHSVVGPPFTGGDL 500

Qy 400 -----YVDSPPQOKYKIYRIANNLASGVSILTYNNQFFFTDILNTSDPNG 447

Db 501 RRTSPGQISTLRKVITAPLSQRVVRIRY-----ASTYNDLF-----HTSIDGR 545

Qy 448 V-RKNGSYTLVEPPIE-----PSGGINIFKLQ-----SQGGEPAIDSIIF 448

Db 546 INQGNF-SATWSSQSNLSQSGFRTVFTFPNFSNGSVFTLSAHVFNSGNEVYIDRIEF 604

Qy 489 SP 490

Db 605 VP 606

RESULT 8

JD0002

paraoporal crystal protein cry1ab3 - *Bacillus thuringiensis*

Nlternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal protein

CtSpecies: *Bacillus thuringiensis*

CtDate: 28-Dec-1987 #sequence, revision 28-Dec-1987 #text, change 09-Jul-2004

CtAccession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002

RtKondo, S.; Tamura, N.; Kunitake, A.; Hattori, M.; Akashi, A.; Ohmori, I.

AgriC. Biol. Chem. 51, 455-463, 1987

ArtTitle: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from *Bacillus thuringiensis*

A.Reference number: A90025

A.Molecule type: mRNA

A.Accession: A90025

A.Molecule type: DNA

A.Residues: 1-1155 <KON>

A.Cross-references: UNIPROT:P06578

A.Experimental source: subsp. kurstaki

RtGeisler, M.; Schweitzer, S.; Grimm, C.

Gene 48, 109-118, 1986

ArtTitle: The hypervariable region in the genes coding for entomopathogenic crystal proteins of *Bacillus thuringiensis*

A.Reference number: A91560; MUID:87163505; PMID:3557124

A.Accession: A91560

A.Molecule type: DNA

A.Residues: 1-1155 <GEI>

A.Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124

A.Experimental source: subsp. kurstaki

RtWabiko, H.; Raymond, K.C.; Bulla Jr., L.A.

DNA 5, 305-314, 1986

ArtTitle: *Bacillus thuringiensis* entomocidal protoxin gene sequence and gene product analysis

A.Reference number: A90955; MUID:86300092; PMID:3743338

A.Accession: A90955

R:Haider, M.Z.; Ellar, D.J.
J. Mol. Biol. 208, 183-194, 1989
A:Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes
A:Reference number: S04994; MUID:89362455; PMID:2769751

A:Accession: S04994

A:Molecule type: DNA

A:Residues: 429-449, 'A', 451-724 <HAM>

A:Cross-references: EMBL:X16315

A:Experimental source: strain aizawai ICI

C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 7.2%; Score 184; DB 2; Length 1155;

Best Local Similarity 20.4%; Pred. No. 2.2e-05;

Matches 121; Conservative 87; Mismatches 187; Indels 198; Gaps 29;

```

QY      8 GVITQFRILNDNFIXIA-----KLFQSTNSDL-----QYPLTLPLR 46
DB      102 GLSNLYQIVASFRFEMADPTNPALREMRIOFNQMSALTTALPLFAVQNYQVPLLSVY 161
QY      47 AQACWMLMLKDATTSVWGQ--IDSQQLNGYKAEILRLIKYTNVDVNTTYNGLELEK 104
DB      162 VQANLHLSTLRD--VSFQGRMGFPDATTINSRYNDLTRIGNYTDHAVRYNTGLE--- 216
QY      105 AKPLNYSDDPEYLQAGRPDISVLRSNFKEVMKMKVAKYKGMMSALSIALAPPTF-GP 163
DB      217 -----RWGPD-----SRDWIRYQFRRLTLTVLDIVSLFPNYSR 253
QY      164 NYPKQALKVQSRQIFA-PVI-----GIPGITSQDSGPTFGSMRFPDKTYDQ 210
DB      254 TYPRTVSQ-LTREITNPVLENFDSFRGSAQIEGSIKSP-----HL 296
QY      211 IDALRLQMLLYIQLKSAFYWIESDKVRATYNDYIGKRGSTGAAMH--MSSDPSA 268
DB      297 MDLINSI-TIYTDHARGEYV--SGHQIMASPV---GFGPEFTFPPLGYTMGNAAPQ 348
QY      269 IYTSALGAGY-----APNVGV-----RSHGGS-----YTKG--- 297
DB      349 RIVAQLOGGVRTLSSTLYRRPFNIGINNQOLSVLDGTEFAVGTSSNLSAIVYKSGTVD 408
QY      298 ---MAPANTNAYAPFEFKYPGKLSAVAGLSKAPDAADSVMGFRPVLLENANQL 353
DB      409 SLDEIPPNQNNVPPROGFS-----HRLSHVSMFSGSNSVSI-IRPMFS----- 454
QY      354 TDTALQIPAEIGITDVPAFGRTTEEPINGQDAIRIWESFTSGFPT----- 399
DB      455 ---WIRSAEFNNIIPSSQITQLPLKSTNLGSGTSVVKGPFGTGDIILRTSPGQIS 509
QY      400 ---YVDSPOKOKYKIIYRIANNLASASTVSLTYNNOTFTDLINSLDPNGV-RGNYGSY 455
DB      510 TLRVAVITAPLSQRYVRIRY-----ASTTNLQ-----LHTSIDGRINQGNF-SA 553
QY      456 TLVEGPILIE-----FSQGTNIFKLG---SQKGEFAIDSIIFS 490
DB      554 TMSGSSNLOGSGFRIVGFTTTPNFNSGVSFTLSAHVNSGNEVYIDRIEFV 606

```

RESULT 13

139838
parasporal crystal protein - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*

C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C:Accession: 139838

R:Hefford, M.A.; Brouseau, R.; Prefontaine, G.; Hanna, Z.; Condie, J.A.; Lau, P.C.K.

J. Biotechnol. 6, 307-322, 1987

A:Title: Sequence of a lepidopteran toxin gene of *Bacillus thuringiensis* subsp. *kurstaki*

A:Reference number: 139838

A:Accession: 139838

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1155 <RES>

A:Cross-references: UNIPROT:P06578; GB:M37263; NID:g142885; PIDN:AAA2420.1; PID:g142886

C:Superfamily: parasporal crystal protein

C:Keywords: delta-endotoxin

Query Match 7.2%; Score 184; DB 2; Length 1155;

Best Local Similarity 20.1%; Pred. No. 2.2e-05;

Matches 121; Conservative 86; Mismatches 180; Indels 214; Gaps 30;

```

QY      8 GVITQFRILNDNFIXIA-----KLFQSTNSDL-----QYPLTLPLR 46
DB      102 GLSNLYQIVASFRFEMADPTNPALREMRIOFNQMSALTTALPLFAVQNYQVPLLSVY 161
QY      47 AQACWMLMLKDATTSVWGQ--IDSQQLNGYKAEILRLIKYTNVDVNTTYNGLELEK 104
DB      162 VQANLHLSTLRD--VSFQGRMGFPDATTINSRYNDLTRIGNYTDHAVRYNTGLE--- 216
QY      105 AKPLNYSDDPEYLQAGRPDISVLRSNFKEVMKMKVAKYKGMMSALSIALAPPTF-GP 163
DB      217 -----RWGPD-----SRDWIRYQFRRLTLTVLDIVSLFPNYSR 253
QY      164 NYPKQALKVQSRQIFA-PVI-----GIPGITSQDSGPTFGSMRFPDKTYDQ 210
DB      254 TYPRTVSQ-LTREITNPVLENFDSFRGSAQIEGSIKSP-----HL 296
QY      211 IDALRLQMLLYIQLKSAFYWIESDKVRATYNDYIGKRGSTGAAMH--MSSDPSA 268
DB      297 MDLINSI-TIYTDHARGEYV--SGHQIMASPV---GFGPEFTFPPLGYTMGNAAPQ 348
QY      269 IYTSALGAGY-----APNVGV-----RSHGGS-----YTKG--- 297
DB      349 RIVAQLOGGVRTLSSTLYRRPFNIGINNQOLSVLDGTEFAVGTSSNLSAIVYKSGTVD 408
QY      298 ---MAPANTNAYAPFEFKY-----PGKLSAVAGLSKAPDAADSVMGFRPVL 344
DB      409 SLDEIPPNQNNVPPROGFSHRLSHVSMFSGSNSVSI-ITAP-----MSSW--- 455
QY      345 LENENQQLTDTALQIPAEIGITDVPAFGRTTEEPINGQDAIRIWESFTSGFPT----- 399
DB      456 IHRSAN-----FNNIIPSSQITQLPLKSTNLGSGTSVVKGPFGTGDIIL 500
QY      400 ---YVDSPOKOKYKIIYRIANNLASASTVSLTYNNOTFTDLINSLDPNG 447
DB      501 RRTSPQISTLRVAVITAPLSQRYVRIRYAST-----TLQFTTSLHGRPIN--- 547
QY      448 VRGVGYSYTLVEGPILIE-----FSQGTNIFKLG---SQKGEFAIDSIIFS 489
DB      548 -QGNF-SATMSSGSSNLOGSGFRHLGFTTTPNFNSGVSFTLSAHVNSGNEVYIDRIEFV 605
QY      490 P 490
DB      606 P 606

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RESULT 14

718212
parasporal crystal protein crysAb1 - *Bacillus thuringiensis* (fragment)

C:Species: *Bacillus thuringiensis*

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: 718212

R:Narva, K.B.; Payne, J.M.; Schwab, G.E.; Hickie, L.A.; Galasas, T.; Sick, A.J.

submitted to the EMBL Data Library, July 1999

A:Description: Novel *Bacillus thuringiensis* microbes active against nematodes, and genes

A:Reference number: Z18829

A:Accession: 718212

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1289 <NAR>

A:Cross-references: UNIPROT:Q45753; EMBL:L07026; NID:g142769; PID:g142770; PIDN:AAA67693

C:Genetics:

A:Gene: CRYVA(b)

C:Keywords: delta-endotoxin

Query Match

Best Local Similarity 20.8%; Score 183.5; DB 2; Length 1289;

Matches 121; Conservative 86; Mismatches 180; Indels 214; Gaps 30;

	Matches	119;	Conservative	87;	Mismatches	212;	Indels	153;	Gaps	30;
OY	7	TGVTTQF--RLINNFRIKIAKLOESTNQSLQPVLTLPRAQAQWHEMLLDADTTS-	63							
Db	176	SGLIKKFTEVDELSNSP-YTDRLPFITDNRADRTLGLPYVALIASHGHLMLLDITTK	234							
OY	64	-VMGQOID--SQOLNGYKAELIRLIKVTYNVNNTYNOGLELEAKPLANSYDPREYLQAG	120							
Db	235	PIMOSKINFETDAIDSEFTDKIKNNIKLXSKITIYDFQGL-----ASYTP-----	280							
OY	121	RPDISVLRSNEKEVWKANKVKAYKRGMASALSLALEPTFGPN-YPKQA-LKVQSRO	177							
Db	281	-----SDLESFAKKQKYIEIMTHHCLDFARLPFPEDPDLYPGSGDISIQKTRR	329							
OY	178	IFAPVIGIPGGITQDSGPTFGSMRFVKTYDQID-----ALRDLMLY----	221							
Db	330	ILSFPIPI----RTADGLTLNNTSIDTSNMPYENGNGAFNPNERILKQ-FKLYPEWR	383							
OY	222	-----IQPLKSAFYMIYESDMKVRATYYN-----DYIGRGSGTGAAMNM--	261							
Db	384	AAQYGGLQP----YLAIEVDQSVETRLYGOQLPRVPDAQAPNYVISDSNPITIIQMNDT	439							
OY	262	WSDDPSALYTSALGAGAYPNVV-----GVRYSS-HGGSYTKGMABANTNAY	306							
Db	440	WKTEPPQ-----GASGMNTNIMRGVSGLSFLORDGRTRLAAGMGGGFADTIYSLPATHY	492							
OY	307	APFEKPYP-----GYKHLSVASGLSKAPDPAADSMMFFRVYLENENOLLTPTALQIP	361							
Db	493	LSYLYGTPEYQSDNMSGHVAGLVGSTPEQEXTLPNIIG-QP-----DEGANST-----	540							
OY	362	AEIGITDVVPAFGRT--EEPINGODAIRIWESFTSGFYTTPVSPQOKOKIITYRIANN	419							
Db	541	--MGPFPFKASVGGIVKEMLGANMAKLSQGSIGIPITVTVSG---EQICRCRAYSN	594							
OY	420	L\$ASTVSLTYNNQT-----FFTDI-LNTSLDPN-GVRGNYSYTL-----VECP	461							
Db	595	--DNITVFENVVDGKANPIFOQINFASFVDNNTGVCQANGVVYKSJATYDNSFTVXIP	651							
OY	462	IIFSOGNINFKLSQKGEPALDSITFSPPV	492							
Db	652	---AKTINVHLTNQGSSDVFUDLRIBFVPIIL	678							

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RESULT 15
T18213
paraporal crystal protein cry5a1 - Bacillus thuringiensis (fragment)
C:Species: Bacillus thuringiensis
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18213
R:Navra, K.E.; Payne, J.M.; Schaab, G.E.; Hickle, L.A.; Galasan, T.; Sick, A.J.
submitted to the EMBL Data Library, July 1999
A:Description: Novel Bacillus thuringiensis microbes active against nematodes, and genes
A:Reference numbers: Z18829
A:Accession: T18213
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1385 <NAR>
A:Cross-references: UNIPROT:Q45760; EMBL:L07025; NID:g142868; PID:g142869;
C:Genetics:
A:Gene: CryVA(a)

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Query Match	7.1%;	Score 183;	DB 2;	Length 1385;
Best Local Similarity	21.1%;	Pred No. 3.5e-05;		
Matches 119;	Conservative 83;	Mismatches 218;	Indels 144;	Gaps 30

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QY      7  GGVLTQF--RIINDNPETKIATLQGFSTNSDQYPLVLTPLRQAQWCHMLILKADTTS- 63
Db      176  SGLIKGFIDEVLSLNSF-YTDRLPVETITDTYADRTLGLGPYYAIIILASHMLMLARDITYG 234
QY      64  -VWGQIID--SOQLNGYKAEILRLIKVYTNDDVNTYNGGLELEKAKPLNSDPEEYLAQG 120
Db      235  PTWDSKINFTPDALISFEKTDIKNNIKLYSKRTIYDVQKGI-----ASQGNP----- 280

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OY      121  RPDISVLRNSFKEMKMNVAKYKKGMMASLSIALAEPFPGPN-YPKOA--LKVVSQ  177
Db      281  -----SDLESFAKKQKIIEIMTHCLDPARLFPFTDPDLVYFTSGSDISLQKTR  329
OY      178  IFAPVIGIPGQITTSQDSGFPFGSMKFDVKTYYDQID-----ALRQMLEY--  221
Db      330  ILSPFIPi-----RTADGLTLNNTSIDTSNPNVENGNGAEPNKEKILKQ-FALYPSMR  383
OY      222  -----IOLPSAWIYIESDMKRYATVYV-----DYIGRKGNSGTGAAMM--  261
Db      384  AGQYGLQD--YMAIEVODSVETRLYGOLPAVDPOAGPNVNSIDSSPII1QINMDT  439
OY      262  WSSDSPAIYTSALGAAGVAPNVY-----GVRYS--HGGSYTKGMAPANTNAY  306
Db      440  WKTRPQ-----GASGMNTLMRGSVSGLSFLQRDGRILASAGGGGADITYSLPATHY  492
OY      307  APEPFKYP---GYLHSVSAIYGLSKAPDAADSMKFRFVYLLENANQLDITLALQIP  361
Db      493  LSLVLYGTPYQTSIDNYSVGHGALVGVSTPOEATLPN1IG-QP-----DQGNVST-----  540
OY      362  AEIGITDVVPAFCRT--EEPINGQDAIRIMESFTSGCFYTYVDSPOKOKYIIRIANN  419
Db      541  --MGFFPEKASVYGTIVYKWLGNANAMLSGQSIGIPITNVTSG-----EQIRCRASN  594
OY      420  LSAVSVSLYVNNOT-----FETDI-LNTSLDPN-GVRGNVGSYTL-----VEGPIIEFQ  467
Db      595  ---DNTNVFENVDTGAMP1FOOINPASTVNNTGQVAGANVYVKS1AATTNDSFTEIPA  651
OY      468  GT-NITPLSGQKEFAIDSIIFSP  490
Db      652  KTIIVHILTMQSSDVVLDR1E1EFP  675

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Search completed: October 19, 2005, 20:18:30
Job time : 44 secs

Job time : 44 secs